

SOURCE mitochondrion Engraulis encrasicolus (European anchovy)
 ORGANISM Engraulis encrasicolus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Clupeomorpha; Clupeiformes;
 Engraulidae; Engraulis.
 REFERENCE 1 (bases 1 to 216)
 AUTHORS Morán, P.
 TITLE Direct Submission
 JOURNAL Submitted (17-DEC-2001) Genetica, Universidad de Vigo, Campus
 Lagoas Marcosende, Vigo 36200, Spain
 FEATURES Location/Qualifiers
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 /organelle="mitochondrion"
 /mol_type="genomic DNA"
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 /trans_table=2
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 /protein_id="AA178336.1"
 /db_xref="GI:18698528"
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 Best Local Similarity 100.0%; Pred. No. 0.18;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TACCATGAGGACAAATATCATCTG 25
 Db 188 TACCATGAGGACAAATATCATCTG 212

gene
 CDS

ORIGIN

Query Match 100.0%; Score 25; DB 5; Length 216;
 Best Local Similarity 100.0%; Pred. No. 0.18;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TACCATGAGGACAAATATCATCTG 25
 Db 188 TACCATGAGGACAAATATCATCTG 212

RESULT 3
 AF145511
 LOCUS
 DEFINITION Melanoplus angustipennis cytochrome b gene, partial cds;
 mitochondrial gene for mitochondrial product.
 ACCESSION AF145511
 VERSION AF145511.1 GI:5918571
 KEYWORDS
 SOURCE mitochondrion Melanoplus angustipennis (narrowwinged sand
 grasshopper)

ORGANISM Melanoplus angustipennis
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
 Acridoidea; Acrididae; Melanoplinae; Melanoplus.
 1 (bases 1 to 258)
 Chapco, W., Kuperus, W.R. and Litzzenberger, G.S.
 Molecular phylogeny of melanoplinae grasshoppers (Orthoptera:
 Acridoidea). The genus Melanoplus
 Ann. Entomol. Soc. Am. 92 (5), 617-623 (1999)
 REFERENCE 2 (bases 1 to 258)
 AUTHORS Chapco, W., Kuperus, W.R. and Litzzenberger, G.S.
 TITLE Direct Submission
 JOURNAL Submitted (23-APR-1999) Biology, University of Regina, 3737 Wascana
 Parkway, Regina, Saskatchewan S4S 0A2, Canada
 FEATURES Location/Qualifiers
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 /organism="Melanoplus angustipennis"
 /organelle="mitochondrion"
 /mol_type="genomic DNA"
 /db_xref="taxon:103631"
 /country="Canada:Saskatchewan"
 /note="whole insect minus gut"
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 /codon_start=3

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 Best Local Similarity 100.0%; Pred. No. 0.18;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TACCATGAGGACAAATATCATCTG 25
 Db 169 TACCATGAGGACAAATATCATCTG 193

RESULT 5
 AF317194
 LOCUS
 DEFINITION Barytettix humphreysi cytochrome b gene, partial cds; mitochondrial
 gene for mitochondrial product.
 ACCESSION AF317194

/transl_table=5
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 /protein_id="AAD56065.1"
 /db_xref="GI:5918637"
 /translation="IIRTHANGASMFICILYHVGRIYGSYMYTHWTMIGTILF
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ORIGIN
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 Best Local Similarity 100.0%; Pred. No. 0.18;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TACCATGAGGACAAATATCATCTG 25
 Db 169 TACCATGAGGACAAATATCATCTG 193

RESULT 4
 AF145531
 LOCUS
 DEFINITION Melanoplus foedus cytochrome b gene, partial cds; mitochondrial
 gene for mitochondrial product.
 ACCESSION AF145531
 VERSION AF145531.1 GI:5918591
 KEYWORDS
 SOURCE mitochondrion Melanoplus foedus
 ORGANISM Melanoplus foedus
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
 Acridoidea; Acrididae; Melanoplinae; Melanoplus.
 1 (bases 1 to 258)
 Chapco, W., Kuperus, W.R. and Litzzenberger, G.S.
 Molecular phylogeny of melanoplinae grasshoppers (Orthoptera:
 Acridoidea). The genus Melanoplus
 Ann. Entomol. Soc. Am. 92 (5), 617-623 (1999)
 REFERENCE 2 (bases 1 to 258)
 AUTHORS Chapco, W., Kuperus, W.R. and Litzzenberger, G.S.
 TITLE Direct Submission
 JOURNAL Submitted (23-APR-1999) Biology, University of Regina, 3737 Wascana
 Parkway, Regina, Saskatchewan S4S 0A2, Canada
 FEATURES Location/Qualifiers
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 /organism="Melanoplus foedus"
 /organelle="mitochondrion"
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 /db_xref="taxon:103642"
 /country="Canada:Alberta"
 /note="whole insect minus gut"
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 /db_xref="GI:5918650"
 /translation="IIRTHANGASMFICILYHVGRIYGSYMYTHWTMIGTILF
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ORIGIN
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 Db 169 TACCATGAGGACAAATATCATCTG 193

RESULT 5
 AF317194
 LOCUS
 DEFINITION Barytettix humphreysi cytochrome b gene, partial cds; mitochondrial
 gene for mitochondrial product.
 ACCESSION AF317194

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VERSION      AF317194.1  GI:33337314
KEYWORDS
SOURCE       mitochondrial Barytettix humphreysi
ORGANISM     Barytettix humphreysi
             Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
             Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
             Acridoidea; Acrididae; Melanoplinae; Barytettix.
REFERENCE    1 (bases 1 to 258)
AUTHORS      Litzenberger, G.S. and Chapco, W.
TITLE        Direct Submission
JOURNAL      Submitted (26-OCT-2000) Department of Biology, University of
             Regina, 3737 Wascana Parkway, Regina, Saskatchewan S4S 0A2, Canada
FEATURES     source
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             /organelle="mitochondrion"
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             /country="USA: Arizona"
             /note="obtained from dried hind femur"
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             /db_xref="GI:33337315"
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Query Match      100.0%; Score 25; DB 3; Length 258;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TACCATGAGGACAAATATCATCTG 25
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Db 169 TACCATGAGGACAAATATCATCTG 193

RESULT 6
LOCUS      AY004180
DEFINITION Parapodisma mikado cytochrome b gene, partial cds; mitochondrial
ACCESSION  AY004180
VERSION     AY004180.1  GI:20451280
KEYWORDS
SOURCE      mitochondrial Parapodisma mikado
ORGANISM    Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
             Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
             Acridoidea; Acrididae; Catantopinae; Parapodisma.
REFERENCE    1 (bases 1 to 258)
AUTHORS      Litzenberger, G. and Chapco, W.
TITLE        Molecular Phylogeny of Selected Eurasian Podismine Grasshoppers
             (Orthoptera: Acrididae)
JOURNAL      Ann. Entomol. Soc. Am. 94 (4), 505-511 (2001)
REFERENCE    2 (bases 1 to 258)
AUTHORS      Litzenberger, G.S. and Chapco, W.
TITLE        Direct Submission
JOURNAL      Submitted (04-JUL-2000) Biology, University of Regina, 3737 Wascana
             Parkway, Regina, Saskatchewan S4S 0A2, Canada
FEATURES     source
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             /organelle="mitochondrion"
             /mol_type="genomic DNA"
             /db_xref="taxon:109888"
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             <1..>258
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LVMATAFMGVLPWGQMSFWGATVITNLLSAIPYLGDLVQ"
ORIGIN
Query Match      100.0%; Score 25; DB 3; Length 258;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TACCATGAGGACAAATATCATCTG 25
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Db 169 TACCATGAGGACAAATATCATCTG 193

RESULT 7
LOCUS      AY004205
DEFINITION Primnoa litoralis cytochrome b gene, partial cds; mitochondrial
ACCESSION  AY004205
VERSION     AY004205.1  GI:20451330
KEYWORDS
SOURCE      mitochondrial Primnoa litoralis
ORGANISM    Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
             Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
             Acridoidea; Acrididae; Catantopinae; Primnoa.
REFERENCE    1 (bases 1 to 258)
AUTHORS      Litzenberger, G. and Chapco, W.
TITLE        Molecular Phylogeny of Selected Eurasian Podismine Grasshoppers
             (Orthoptera: Acrididae)
JOURNAL      Ann. Entomol. Soc. Am. 94 (4), 505-511 (2001)
REFERENCE    2 (bases 1 to 258)
AUTHORS      Litzenberger, G.S. and Chapco, W.
TITLE        Direct Submission
JOURNAL      Submitted (04-JUL-2000) Biology, University of Regina, 3737 Wascana
             Parkway, Regina, Saskatchewan S4S 0A2, Canada
FEATURES     source
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             /country="Russia"
             /note="from Novosibirsk State University"
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             /db_xref="GI:20451331"
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Query Match      100.0%; Score 25; DB 3; Length 258;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TACCATGAGGACAAATATCATCTG 25
    ||||||||||||||||||
Db 169 TACCATGAGGACAAATATCATCTG 193

RESULT 8
LOCUS      CCU17904
DEFINITION Circotettix carlinianus mitochondrial cytochrome b gene, partial
             cds.

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ACCESSION      U17904
KEYWORDS       U17904.1 GI:601796
SOURCE         mitochondrial Aereochoereutes carlinianus
ORGANISM       Aereochoereutes carlinianus
               Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
               Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
               Acridoidea; Acrididae; Oedipodinae; Aereochoereutes.
REFERENCE      1 (bases 1 to 258)
AUTHORS       Chapco,W. and Martel,R.K.B.
TITLE         Mitochondrial DNA sequence variation in North American hand-winged
               grasshoppers
JOURNAL        Unpublished
REFERENCE      2 (bases 1 to 258)
AUTHORS       Chapco,W.
TITLE         Direct Submission
JOURNAL        Submitted (01-DEC-1994) Chapco W., University of Regina, Biology,
               Regina, Saskatchewan, Canada, S4S 0A2
               Location/Qualifiers
FEATURES       1..258
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               /dev_stage="adult"
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               /db_xref="GI:601797"
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ORIGIN
Query Match      100.0%; Score 25; DB 3; Length 258;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TACCATGAGGACAAATATCATCTG 25
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DB      169 TACCATGAGGACAAATATCATCTG 193

RESULT 10
LOCUS      SCU18257          258 bp    DNA    linear    INV 27-JAN-1995
DEFINITION Sparagemon collare cytochrome b gene, mitochondrial gene encoding
               mitochondrial protein, partial cds.
ACCESSION   U18257
VERSION     U18257.1 GI:624181
KEYWORDS    .
SOURCE      mitochondrion Sparagemon collare (mottled sand grasshopper)
ORGANISM    Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
               Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
               Acridoidea; Acrididae; Oedipodinae; Sparagemon.
REFERENCE   1 (bases 1 to 258)
AUTHORS     Chapco,W. and Martel,R.K.B.
TITLE       Mitochondrial DNA sequence variation in North American band-winged
               grasshoppers
JOURNAL      Unpublished
REFERENCE    2 (bases 1 to 258)
AUTHORS     Chapco,W.
TITLE       Direct Submission
JOURNAL      Submitted (06-DEC-1994) William Chapco, University of Regina,
               Biology, Regina, Saskatchewan, S4S 0A2, Canada
               Location/Qualifiers
FEATURES     1..258
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               /dev_stage="adult"
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               /product="cytochrome b"
               /protein_id="AAA61678.1"
               /db_xref="GI:624182"
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ORIGIN
Query Match      100.0%; Score 25; DB 3; Length 258;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TACCATGAGGACAAATATCATCTG 25
        |||||||
DB      169 TACCATGAGGACAAATATCATCTG 193

RESULT 9
CPUI8250
LOCUS      CPU18250          258 bp    DNA    linear    INV 27-JAN-1995
DEFINITION Cammulla pellucida cytochrome b gene, mitochondrial gene encoding
               mitochondrial protein, partial cds.
ACCESSION   U18250
VERSION     U18250.1 GI:624167
KEYWORDS    .
SOURCE      mitochondrion Cammulla pellucida (clear-winged grasshopper)
ORGANISM    Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
               Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
               Acridoidea; Acrididae; Oedipodinae; Cammulla.
REFERENCE   1 (bases 1 to 258)
AUTHORS     Chapco,W. and Martel,R.K.B.
TITLE       Mitochondrial DNA sequence variation in North American band-winged
               grasshoppers
JOURNAL      Unpublished
REFERENCE    2 (bases 1 to 258)
AUTHORS     Chapco,W.
TITLE       Direct Submission
JOURNAL      Submitted (06-DEC-1994) William Chapco, University of Regina,
               Biology, Regina, Saskatchewan, S4S 0A2, Canada
               Location/Qualifiers
FEATURES     1..258
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               /organelle="mitochondrion"

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RESULT 11
SCU18258
LOCUS
DEFINITION
Spharagemon campestris cytochrome b gene, mitochondrial gene
ACCESSION
U18258
VERSION
U18258.1 GI:624183
KEYWORDS
mitochondrion Spharagemon campestris
SOURCE
Spharagemon campestris
ORGANISM
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
Acridoidea; Acrididae; Oedipodinae; Spharagemon.
REFERENCE
AUTHORS
Chapco,W. and Martel,R.K.B.
TITLE
Mitochondrial DNA sequence variation in North American band-winged
grasshoppers
JOURNAL
Unpublished
REFERENCE
2 (bases 1 to 258)
AUTHORS
Chapco,W.
TITLE
Direct Submission
JOURNAL
Submitted (06-DEC-1994) William Chapco, University of Regina,
Biology, Regina, Saskatchewan, S4S 0A2, Canada
FEATURES
source
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/organism="Spharagemon campestris"
/organelle="mitochondrion"
/mol_type="genomic DNA"
/isolate="Last Mountain Lake, Saskatchewan"
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ORIGIN
Query Match 100.0%; Score 25; DB 3; Length 258;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TACCATGAGGACAAATATCATCTG 25
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Db 169 TACCATGAGGACAAATATCATCTG 193

RESULT 12
TPU18253
LOCUS
DEFINITION
Trimerotropis pistrinaria cytochrome b gene, mitochondrial gene
ACCESSION
U18253
VERSION
U18253.1 GI:624173
KEYWORDS
mitochondrion Trimerotropis pistrinaria
SOURCE
Trimerotropis pistrinaria
ORGANISM
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
Acridoidea; Acrididae; Oedipodinae; Trimerotropis.
REFERENCE
AUTHORS
Chapco,W. and Martel,R.K.B.
TITLE
Mitochondrial DNA sequence variation in North American band-winged
grasshoppers
JOURNAL
Unpublished
REFERENCE
2 (bases 1 to 258)
AUTHORS
Chapco,W.
TITLE
Direct Submission
JOURNAL
Submitted (06-DEC-1994) William Chapco, University of Regina,
Biology, Regina, Saskatchewan, S4S 0A2, Canada
FEATURES
source
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/organism="Spharagemon campestris"
/organelle="mitochondrion"
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/isolate="Last Mountain Lake, Saskatchewan"
/db_xref="taxon:37256"
/tissue_type="whole organism minus gut"
/dev_stage="adult"
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/codon_start=3
/transl_table=5
/product="cytochrome b"
/protein_id="AA61679.1"
/db_xref="GI:624184"
/translation="IIRTHANGAMLFFICIVLHVGRGIYGSYMYMTWMTGTWMLF
LVMTAFMGYVLPWGQMSFWGATVITNLLSAIPYMGTEIVQ"

ORIGIN
Query Match 100.0%; Score 25; DB 3; Length 258;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TACCATGAGGACAAATATCATCTG 25
|||||
Db 169 TACCATGAGGACAAATATCATCTG 193

RESULT 13
AF371961
LOCUS
DEFINITION
Bos taurus cytochrome b (cytb) gene, partial cds; mitochondrial
gene for mitochondrial product.
ACCESSION
AF371961
VERSION
AF371961.1 GI:14091672
KEYWORDS
mitochondrion Bos taurus (cow)
SOURCE
Bos taurus
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
REFERENCE
AUTHORS
Bottero,M.T., Civera,T., Anastasio,A., Turi,R.M. and Rosati,S.
TITLE
Identification of cow's milk in 'buffalo' cheese by duplex
polymerase chain reaction
JOURNAL
J. Food Prot. 65 (2), 362-366 (2002)
MEDLINE
21837100
PUBMED
11848568
REFERENCE
2 (bases 1 to 279)
AUTHORS
Bottero,M.T. and Rosati,S.
TITLE
Direct Submission
JOURNAL
Submitted (18-APR-2001) Produzioni Animali, Facolta' di Medicina
Veterinaria, Via Nizza, 52, Torino, TO 10126, Italy
FEATURES
source
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/organism="Bos taurus"
/organelle="mitochondrion"
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/transl_table=2
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/protein_id="AAK53817.1"
/db_xref="GI:14091673"
/translation="GLYSGSYTFLETWNIGVILLTVMATFAFMGYVLPWGQMSFWGAT
VITNLLSAIPYIGTNLVEWGWGSKATLTFFAHFILPFIIMAA"

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ORIGIN

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 Matches 25; Conservative 0; Mismatches 0;

Qy 1 TACCATGAGGACAAATATCATCTG 25
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Db 98 TACCATGAGGACAAATATCATCTG 122
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RESULT 14

S49215 279 bp DNA linear MAM 05-AUG-1999
 LOCUS apocytochrome b [sheep, domestic, Merinolandschaf, liver,
 DEFINITION Mitochondrial, 279 nt].

ACCESSION S49215 GI:259294

KEYWORDS

SOURCE

ORGANISM

mitochondrion Ovis aries (sheep)

Ovis aries

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Caprinae; Ovis.

REFERENCE 1 (bases 1 to 279)

AUTHORS Hiedler, S., Hecht, W., Dzapo, V. and Wassmuth, R.

TITLE Ovine mitochondrial DNA: restriction enzyme analysis, mapping and
 sequencing data

JOURNAL Anim. Genet. 23 (2), 151-160 (1992)

MEDLINE 93073120

PUBMED 1332554

REMARK GenBank staff at the National Library of Medicine created this
 entry [NCBI gibseq 117456] from the original journal article.

FEATURES

source

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/organism="Ovis aries"

/organelle="mitochondrion"

/mol_type="genomic DNA"

/db_xref="taxon:9940"

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/gene="Cyt.b"

<1..>279

/gene="Cyt.b"

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/transl_table=2

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/protein_id="AAB24056.1"

/db_xref="GI:259295"

/translation="IGVILLFATWATPMGVLPWQMSFWGATVITNLLSAIPYIGT
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ORIGIN

Query Match 100.0%; Score 25; DB 4; Length 279;
 Best Local Similarity 100.0%; Pred. No. 0.18; 0; Indels 0; Gaps 0;
 Matches 25; Conservative 0; Mismatches 0;

Qy 1 TACCATGAGGACAAATATCATCTG 25
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Db 56 TACCATGAGGACAAATATCATCTG 80
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RESULT 15

AY217671

LOCUS

DEFINITION Xenopus laevis isolate 3 from South Africa cytochrome b (cytb)
 mRNA, partial cds; mitochondrial gene for mitochondrial product.

ACCESSION AY217671

VERSION AY217671.1 GI:31322351

KEYWORDS

SOURCE

ORGANISM

mitochondrion Xenopus laevis (African clawed frog)

Xenopus laevis

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae;

REFERENCE

1 (bases 1 to 290)

AUTHORS Measey, J. and Channing, A.

TITLE Phylogeography of the genus Xenopus in southern Africa

JOURNAL Amphib-reptil. (2003) In press

REFERENCE 2 (bases 1 to 290)

AUTHORS Measey, J.

TITLE Direct Submission

JOURNAL Submitted (11-JAN-2003) Dept. Zoology, University of the Western
 Cape, Private Bag X17, Bellville 7535, South Africa

FEATURES

source

1..290

/organism="Xenopus laevis"

/organelle="mitochondrion"

/mol_type="mRNA"

/isolate="J3"

/db_xref="taxon:8355"

/country="South Africa: Pearly Beach"

/note="isolated by JM & AC"

<1..>290

/gene="cytb"

<1..>290

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/codon_start=3

/transl_table=2

/product="cytochrome b"

/protein_id="AAP21010.1"

/db_xref="GI:31322352"

/translation="TGLFLAMHYTADTSMAFSSVAHICRDVNYGWLIRNLHANGASPF
 FICILYHIGRGLYGSFLYKETWNIGVILLFLVNATAFVGVLPGQMSFWG"

ORIGIN

Query Match 100.0%; Score 25; DB 5; Length 290;
 Best Local Similarity 100.0%; Pred. No. 0.18; 0; Indels 0; Gaps 0;
 Matches 25; Conservative 0; Mismatches 0;

Qy 1 TACCATGAGGACAAATATCATCTG 25
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Db 262 TACCATGAGGACAAATATCATCTG 286
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Search completed: November 17, 2004, 02:58:37
 Job time : 138.759 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 16, 2004, 22:24:28 ; Search time 357.388 Seconds
(without alignments)
2650.992 Million cell updates/sec

Title: US-09-821-782E-2

Perfect score: 26

Sequence: 1 cctcctagttttagggattgatcg 26

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_hic:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	24.4	93.8	132	2	BE487586 176420 BA
C 2	24.4	93.8	147	7	CR383176 CR383176
C 3	24.4	93.8	188	6	CB226256 IRT31H03
C 4	24.4	93.8	250	6	CB227362 IRT31H03
C 5	24.4	93.8	256	6	CB221363 IRT31H03
C 6	24.4	93.8	293	6	CD288296 3 P21.abd
C 7	24.4	93.8	300	7	CK959074 4059657 B
C 8	24.4	93.8	304	4	BM434693 IRT11H08
C 9	24.4	93.8	322	4	BM434895 IRT15D07
C 10	24.4	93.8	324	4	BI538794 434369 MA
C 11	24.4	93.8	328	1	AJ693580 AJ693580
C 12	24.4	93.8	330	4	BM435757 IRT31H03
C 13	24.4	93.8	330	7	CK727400 UMC-bend
C 14	24.4	93.8	331	2	BE487585 176419 BA
C 15	24.4	93.8	331	7	CN998120 UMC-bcl_0
C 16	24.4	93.8	333	2	BF429485 1014 MARC
C 17	24.4	93.8	333	7	CK729034 UMC-bend
C 18	24.4	93.8	338	4	BM435844 IRT5A12_a
C 19	24.4	93.8	339	7	CN654035 UMC-bcl_0
C 20	24.4	93.8	342	2	BF429697 1465 MARC
C 21	24.4	93.8	342	5	BF103466 BPI03466
C 22	24.4	93.8	343	4	BM434542 IRT06A12
C 23	24.4	93.8	344	7	CK728189 UMC-bcl_0
C 24	24.4	93.8	344	7	CN653932 UMC-bcl_0

25	24.4	93.8	344	7	CO000574
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27	24.4	93.8	347	7	CO727212
28	24.4	93.8	348	4	BM434469
29	24.4	93.8	351	7	CN654069
30	24.4	93.8	351	7	CO000322
31	24.4	93.8	353	7	CN654050
32	24.4	93.8	353	7	CO728674
33	24.4	93.8	354	7	CN999365
34	24.4	93.8	355	6	CB226824
35	24.4	93.8	355	7	CK729003
36	24.4	93.8	356	5	BP102696
37	24.4	93.8	356	7	CN654406
38	24.4	93.8	357	6	CB226333
39	24.4	93.8	358	1	AU277856
40	24.4	93.8	358	5	BP109501
41	24.4	93.8	359	7	CK983106
42	24.4	93.8	360	4	BM434466
43	24.4	93.8	360	4	BM436089
44	24.4	93.8	360	7	CK729336
45	24.4	93.8	362	4	BM436122

ALIGNMENTS

RESULT 1
BE487586/c
LOCUS BE487586 176420 BAC 5BOV Bos taurus cDNA 5', mRNA linear EST 27-MAR-2003
ACCESSION BE487586
VERSION BE487586.1 GI:9607119
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 132)
AUTHORS Sonstegard,T., Capuco,A.V., White,J., Van Tassel,C.P., Connor,E.E., Cho,J., Sultana,R., Shade,L., Wray,J.E., Wells,K.D. and Quackenbush,J.
TITLE Analysis of bovine mammary gland EST and functional annotation of the Bos taurus gene index
JOURNAL Mamm. Genome 13 (7), 373-379 (2002)
MEDLINE 22135956
PUBMED 12140684
COMMENT Contact: Sonstegard TS
USDA, ARS, Beltsville Agricultural Research Center
Bldg. 200 Rm 2A, Beltsville, MD 20705, USA
Tel: 301 504 8416
Fax: 301 504 8414
Email: tad@psi.barc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -mismatch 12 options.
PCR Primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCCTCAGTCACGACG
Plate: 138 row: M column: 10
Seq primer: ATTAGTGACACTATAG.

FEATURES

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/tissue_type="pooled"
/lab_host="DH10B"
/clone_lib="BAC 5BOV"
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ORIGIN
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Best Local Similarity 96.2%; Pred. No. 1;
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCTCCTAGTTTGTAGGATTCG 26
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Db 61 CCTCCTAGTTTGTGGGATTCG 36

RESULT 2
CR383176/c
LOCUS CR383176 147 bp mRNA linear EST 04-MAY-2004
DEFINITION CR383176 Bovine multi-stage muscles library (bcas) Bos taurus cDNA
clone bcas0003a.f.03 5prim, mRNA sequence.
ACCESSION CR383176
VERSION CR383176.1 GI:47005080
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
REFERENCE 1 (bases 1 to 147)
AUTHORS Chevalet, C.
TITLE AGENAE, a French Animal Genome project
JOURNAL Unpublished (2004)
COMMENT Contact: Martin P
INRA, Genomique & Physiologie de la Lactation
Domaine de Vilvert, 78352 JOUY-EN-JOSAS cedex, FRANCE
Tel: +33 (0) 1.34.65.25.82
Fax: +33 (0) 1.34.65.29.26
Email: Patrice.Martin@jouy.inra.fr
Sequence cleaned of vector, adaptor and repetitions. Contact us
at signenasupport@jouy.inra.fr to obtain the chromatogram of this
sequence.
Plate: 0003 row: f column: 3.
FEATURES
Location/Qualifiers
1..147
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/mol_type="mRNA"
/db_xref="taxon:9913"
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semitendinosus, masseter, cutaneous trunci"
/dev_stages="from embryos to adults"
/clone_lib="Bovine multi-stage muscles library (bcas)"
/note="Clone distribution : AGENAE Resource centre.
Francois PIUMI, Francois.Piumi@jouy.inra.fr, INRA, CEA
Radiobiologie et Etude du genome (LREG), Domaine de
Vilvert, 78352, Jouy-en-Josas cedex, FRANCE, +33 (0)
1.34.65.28.02, +33 (0) 1.34.65.22.73"

ORIGIN
Query Match          93.8%; Score 24.4; DB 7; Length 147;
Best Local Similarity 96.2%; Pred. No. 1;
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCTCCTAGTTTGTAGGATTCG 26
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Db 65 CCTCCTAGTTTGTGGGATTCG 40

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CB226256/c
LOCUS CB226256 198 bp mRNA linear EST 10-FEB-2003
DEFINITION CB226256 Bos taurus Reticulum #1 library Bos taurus cDNA, mRNA
sequence.
ACCESSION CB226256
VERSION CB226256.1 GI:28296770
KEYWORDS EST.
SOURCE Bos taurus (cow)

ORIGIN
Query Match          93.8%; Score 24.4; DB 6; Length 188;
Best Local Similarity 96.2%; Pred. No. 1.1;
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCTCCTAGTTTGTAGGATTCG 26
|||||
Db 158 CCTCCTAGTTTGTGGGATTCG 133

RESULT 4
CB227362/c
LOCUS CB227362 250 bp mRNA linear EST 10-FEB-2003
DEFINITION CB227362 Bos taurus Rumen #1 library Bos taurus cDNA, mRNA
sequence.
ACCESSION CB227362
VERSION CB227362.1 GI:28297876
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
REFERENCE 1 (bases 1 to 250)
AUTHORS Hansen, C., Fu, A., Meng, Y., Li, C., Okine, E., Sensen, C.W.,
Gordon, P.M.K. and Moore, S.S.
TITLE Gene Expression Profiling of the Bovine Gastrointestinal Tract
JOURNAL Unpublished (2002)
COMMENT Contact: Dr. Stephen Moore
Beef Genomics Laboratory
Dept of AFNS, University of Alberta
410 Agri/For, Dept of AFNS, U of A, Edmonton, AB, T6G 2P5, Canada
Tel: 780 492 0169
Fax: 780 492 4285
Email: stephen.moore@ualberta.ca
Insert Length: 250 Std Error: 0.00
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FEATURES
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EcoRI; Site_2: Xho I"

ORIGIN
Query Match          93.8%; Score 24.4; DB 6; Length 188;
Best Local Similarity 96.2%; Pred. No. 1.1;
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCTCCTAGTTTGTAGGATTCG 26
|||||
Db 158 CCTCCTAGTTTGTGGGATTCG 133

RESULT 4
CB227362/c
LOCUS CB227362 250 bp mRNA linear EST 10-FEB-2003
DEFINITION CB227362 Bos taurus Rumen #1 library Bos taurus cDNA, mRNA
sequence.
ACCESSION CB227362
VERSION CB227362.1 GI:28297876
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
REFERENCE 1 (bases 1 to 250)
AUTHORS Hansen, C., Fu, A., Meng, Y., Li, C., Okine, E., Sensen, C.W.,
Gordon, P.M.K. and Moore, S.S.
TITLE Gene Expression Profiling of the Bovine Gastrointestinal Tract
JOURNAL Unpublished (2002)
COMMENT Contact: Dr. Stephen Moore
Beef Genomics Laboratory
Dept of AFNS, University of Alberta
410 Agri/For, Dept of AFNS, U of A, Edmonton, AB, T6G 2P5, Canada
Tel: 780 492 0169
Fax: 780 492 4285
Email: stephen.moore@ualberta.ca
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FEATURES
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9913"

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/cell_type="Stratified squamous epithelial"
/dev_stage="Young adult"
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/clone_lib="Bos taurus Rumex #1 library"
/notes="Organ: Rumex; Vector: Uni-2ZAPXR; Site_1: EcoRI;
Site_2: Xho I"

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Best Local Similarity 96.2%; Pred. No. 1.1;
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCTCCTAGTTTGTAGGATTGATCG 26
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Db 74 CCTCCTAGTTTGTGGGATTGATCG 49

RESULT 5
CB221363/c
LOCUS CB221363 256 bp mRNA linear EST 10-FEB-2003
DEFINITION ldu05f04 Bos taurus Duodenum #1 library Bos taurus cDNA, mRNA
sequence.
ACCESSION CB221363
VERSION CB221363.1 GI:28291877
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
REFERENCE 1 (bases 1 to 256)
AUTHORS Hansen,C., Fu,A., Meng,Y., Li,C., Okine,E., Sensen,C.W.,
Gordon,P.M.K. and Moore,S.S.
TITLE Gene Expression Profiling of the Bovine Gastrointestinal Tract
JOURNAL Unpublished (2002)
COMMENT Contact: Dr. Stephen Moore
Beef Genomics Laboratory
Dept of AFNS, University of Alberta
410 Agri/For, Dept of AFNS, U of A, Edmonton, AB, T6G 2P5, Canada
Tel: 780 492 0169
Fax: 780 492 4265
Email: stephen.moore@ualberta.ca
Insert Length: 256 Std Error: 0.00
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1..256
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/lab_host="XLI-BlueMRF strain"
/clone_lib="Bos taurus Duodenum #1 library"
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Site_1: EcoRI; Site_2: Xho I"

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Best Local Similarity 96.2%; Pred. No. 1.1;
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCTCCTAGTTTGTAGGATTGATCG 26
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Db 154 CCTCCTAGTTTGTGGGATTGATCG 129

RESULT 6
CD288296
LOCUS CD288296 293 bp mRNA linear EST 27-MAY-2003
DEFINITION 3 P21.abd POE14 (Day_14_pregnant_ovine_endometrium) Ovis aries
cDNA, mRNA sequence.

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ACCESSION CD288296
VERSION CD288296.1 GI:31086339
KEYWORDS Ovis aries (sheep)
SOURCE Ovis aries
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Caprinae; Ovis.
REFERENCE 1 (bases 1 to 293)
AUTHORS Gray,C.A., Adelson,D.L. and Spencer,T.E.
TITLE Ovine ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Thomas E. Spencer
Center for Animal Biotechnology and Genomics
Texas A&M University
Animal Science Dept., TAMU-2471, College Station, TX 77843-2471,
USA
Tel: 9798454896
Fax: 9798622662
Email: tspencer@ansc.tamu.edu.
Location/Qualifiers
1..293
/organism="Ovis aries"
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/db_xref="taxon:9940"
/sex="Female"
/tissue_type="endometrium"
/dev_stage="Day 14 pregnant"
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/notes="Organ: uterus; Vector: Triplex2; Site_1: EcoRI;
Site_2: XhoI; Non-normalized library, sequenced 5' with
Triplex2 primer (CTCCGAGATCTGGAGCAGC). Library constructed
by Clontech with total RNA extracted using the Trizol
method and pooled from 5 females."

ORIGIN
Query Match          93.8%; Score 24.4; DB 6; Length 293;
Best Local Similarity 96.2%; Pred. No. 1.1;
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTCTCTAGTTTGTAGGATTGATCG 26
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Db 187 CTCTCTAGTTTATTAGGATTGATCG 212

RESULT 7
CK959074
LOCUS CK959074 300 bp mRNA linear EST 15-MAR-2004
DEFINITION 409657 BARC 10BOV Bos taurus cDNA clone 10BOV6_A24 3', mRNA
sequence.
ACCESSION CK959074
VERSION CK959074.1 GI:45473454
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
REFERENCE 1 (bases 1 to 300)
AUTHORS Sonstegard, T.S., Van Tassel, C.P., Matukumalli, L.K., Harhay,
G.P., Bosak, S., Rubenfield, M. and Gasbarre, L.C.
TITLE Production of EST from cDNA libraries derived from immunologically
activated bovine gut
JOURNAL Unpublished (2004)
COMMENT Contact: Tad S. Sonstegard
Bovine Functional Genomics Laboratory
Animal and Natural Resources Institute
Bldg. 200 Rm2A BARC-East, Beltsville, MD 20705, USA
Tel: 3015048416
Fax: 3015048414
Email: tad@anri.barc.usda.gov
Single pass sequencing. Bases called and trimmed with phred
0.000925 using options -trim_alt " -trim_fasta. Vector identified

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by cross match using options -minmatch 12 -minscore 12
 Plate: 6_row: A column: 24
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FEATURES

Location/Qualifiers
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 /clone_lib="BARC 10BOV"

/note="Organ: Small Intestine; Vector: pAgen-1; Site:1;
 EcorV; Site 2: NotI; Equimolar amounts of mRNA extracted
 from proximal jejunums of 18 and 21 wk old steers, and
 distal ileums of 14 day old calves, proximal jejunum
 exposed to C. oncophora for 3 and 6 weeks, and distal
 ileum exposed to C. parvum for 7 days"

ORIGIN

Query Match 93.8%; Score 24.4; DB 7; Length 300;
 Best Local Similarity 96.2%; Pred. No. 1.1;
 Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCTCCTAGTTTGTAGGATTCATCG 26
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 Db 275 CCTCCTAGTTTGTGGGGATTCATCG 300

RESULT 8

BM434693/c 304 bp mRNA linear EST 31-JAN-2002
 LOCUS 1R11H08 Bos taurus Reticulum #1 library Bos taurus cDNA, mRNA
 DEFINITION

ACCESSION BM434693
 VERSION BM434693.1 GI:18456415

KEYWORDS

SOURCE EST.

ORGANISM

Bos taurus (cow)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovinae; Bos.

1 (bases 1 to 304)

Hansen, C., Fu, A., Meng, Y., Li, C., Okine, E., Sensen, C.W.,
 Gordon, P.M.K. and Moore, S.S.

Gene Expression Profiling of the Bovine Gastrointestinal Tract
 Unpublished (2002)

Contact: Dr. Stephen Moore

Beef Genomics Laboratory

Dept of AFNS, University of Alberta

410 Agri/For, Dept of AFNS, U of A, Edmonton, AB, T6G 2P5, Canada

Tel: 780 492 0169

Fax: 780 492 4265

Email: stephen.moore@ualberta.ca

Insert Length: 304 Std Error: 0.00

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Location/Qualifiers

1..304

/organism="Bos taurus"

/mol_type="mRNA"

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/lab_host="XLI-BlueMRF'strain"

/clone_lib="Bos taurus Reticulum #1 library"

/note="Organ: Reticulum; Vector: Uni-ZAPXR; Site_1:

EcorI; Site_2: Xho I"

ORIGIN

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 Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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|||||

Db 50 CCTCCTAGTTTGTGGGATTCATCG 25

RESULT 9

BM434895/c

LOCUS 1R15007 Bos taurus Reticulum #1 library Bos taurus cDNA, mRNA

DEFINITION

ACCESSION BM434895

VERSION BM434895.1 GI:18456617

KEYWORDS EST.

SOURCE Bos taurus (cow)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovinae; Bos.

1 (bases 1 to 322)

Hansen, C., Fu, A., Meng, Y., Li, C., Okine, E., Sensen, C.W.,

Gordon, P.M.K. and Moore, S.S.

Gene Expression Profiling of the Bovine Gastrointestinal Tract

Unpublished (2002)

Contact: Dr. Stephen Moore

Beef Genomics Laboratory

Dept of AFNS, University of Alberta

410 Agri/For, Dept of AFNS, U of A, Edmonton, AB, T6G 2P5, Canada

Tel: 780 492 0169

Fax: 780 492 4265

Email: stephen.moore@ualberta.ca

Insert Length: 322 Std Error: 0.00

POLYA=No.

Location/Qualifiers

1..322

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/lab_host="XLI-BlueMRF'strain"

/clone_lib="Bos taurus Reticulum #1 library"

/note="Organ: Reticulum; Vector: Uni-ZAPXR; Site_1:

EcorI; Site_2: Xho I"

ORIGIN

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 Best Local Similarity 96.2%; Pred. No. 1.1;
 Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCTCCTAGTTTGTAGGATTCATCG 26

|||||

Db 222 CCTCCTAGTTTGTGGGATTCATCG 197

RESULT 10

BI538794/c

LOCUS BI538794 324 bp mRNA linear EST 30-AUG-2001

DEFINITION 434369 MARC 4BOV Bos taurus cDNA 5', mRNA sequence.

ACCESSION BI538794

VERSION BI538794.1 GI:15379904

KEYWORDS EST.

SOURCE Bos taurus (cow)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovinae; Bos.

1 (bases 1 to 324)

AUTHORS
 Smith, T.P.L., Grosse, W.M., Preking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Perte, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J., and Keele, J.W.
TITLE
 Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle
JOURNAL
 Genome Res. 11 (4), 626-630 (2001)
MEDLINE
 21180013
PUBMED
 11282978
COMMENT
 Contact: Smith TPL
 USDA, ARS, US Meat Animal Research Center
 PO Box 166, Clay Center, NE 68933-0166, USA
 Tel: 402 762 4366
 Fax: 402 762 4390
 Email: smith@email.marc.usda.gov
 Single pass sequencing. Bases called and alt trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options.
 PCR Primers
 FORWARD: AGGAACAGCTATGACCAT
 BACKWARD: GTTTCCTCCAGTCACGACG
 Plate: 137 row: P column: 3
 Seq primer: ATTAGTGACACTATAG.
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 /mol_type="mRNA"
 /db_xref="taxon:9913"
 /tissue_type="pooled"
 /lab_host="DH10B"
 /clone_lib="MARC 4BOV"
 /notes="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI; Library made from pooled tissue from day 20 and day 40 embryos."
ORIGIN
 Query Match 93.8%; Score 24.4; DB 4; Length 324;
 Best Local Similarity 96.2%; Pred. No. 1.1;
 Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CCTCCTAGTTTGTAGGGATTGATCG 26
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 Db 50 CCTCCTAGTTTGTGGGGATTGATCG 25
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 RESULT 11
 AJ693580/c 328 bp mRNA linear EST 29-JUN-2004
 LOCUS
 DEFINITION
 AJ693580 KN261 Bos taurus cDNA clone KN261-041_K22, mRNA sequence.
 ACCESSION
 AJ693580
 VERSION
 AJ693580.1 GI:49426999
 KEYWORDS
 EST.
 SOURCE
 Bos taurus (cow)
 ORGANISM
 Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovinae; Bos.
 REFERENCE
 1 (bases 1 to 328)
 Anderson, S.I., Finlayson, H.A. and Archibald, A.L.
 Development of cDNA and EST resources for studying reproduction and embryo development in pigs and cattle
 Unpublished (2004)
 Contact: Anderson SI
 Genomics and Bioinformatics
 Roslin Institute
 Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
 Single pass sequencing. Bases called and trimmed with phred v0.020425.c. Vector identified by cross_match with the -minscore 20 and -minmatch 12 options. Vector:pBlueScriptII (SK+) R. Site1: EcoRI R. Site2: SmaI 5', Seq Primer T3 Normalised library constructed from bovine ovary. Clones available from UK Centre for Functional Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK,

FEATURES
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 1..328
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 /db_xref="taxon:9913"
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 /tissue_type="ovary"
 /clone_lib="KN261"
 /notes="Vector: pBlueScriptII (SK+); Site 1: EcoRI; Site 2: SmaI; Single pass sequencing. Normalised library constructed from bovine ovary."
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 Best Local Similarity 96.2%; Pred. No. 1.1;
 Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CCTCCTAGTTTGTAGGGATTGATCG 26
 |||||
 Db 57 CCTCCTAGTTTGTGGGGATTGATCG 32
 |||||
 RESULT 12
 BM435757/c 330 bp mRNA linear EST 31-JAN-2002
 LOCUS
 DEFINITION
 BM435757 1RU3C3.ab1 Bos taurus Rumen #1 library Bos taurus cDNA, mRNA sequence.
 ACCESSION
 BM435757
 VERSION
 BM435757.1 GI:18457479
 KEYWORDS
 EST.
 SOURCE
 Bos taurus (cow)
 ORGANISM
 Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovinae; Bos.
 REFERENCE
 1 (bases 1 to 330)
 Hansen, C., Fu, A., Meng, Y., Li, C., Okine, E., Sensen, C.W., Gordon, P.M.K. and Moore, S.S.
 Gene Expression Profiling of the Bovine Gastrointestinal Tract
 Unpublished (2002)
 Contact: Dr. Stephen Moore
 Beef Genomics Laboratory
 Dept of AFNS, University of Alberta
 410 Agri/For, Dept of AFNS, U of A, Edmonton, AB, T6G 2P5, Canada
 Tel: 780 492 0169
 Fax: 780 492 4265
 Email: stephen.moore@ualberta.ca
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 /call_type="Stratified squamous epithelial"
 /dev_stage="Young adult"
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 /clone_lib="Bos taurus Rumen #1 library"
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 Best Local Similarity 96.2%; Pred. No. 1.1;
 Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CCTCCTAGTTTGTAGGGATTGATCG 26
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 Db 62 CCTCCTAGTTTGTGGGGATTGATCG 37
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RESULT 13
 CK727400
 LOCUS UMC-bend_0A01-006-d11 Day 5 Uterus bend Bos taurus cDNA 3', mRNA
 DEFINITION
 ACCESSION CK727400
 VERSION CK727400.1 GI:42580914
 KEYWORDS EST.
 SOURCE Bos taurus (cow)
 ORGANISM Bos taurus
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.
 1 (bases 1 to 330)
 Prather, R.S., Antoniou, E., Garverick, H.A., Green, J.A., Lucy, M.C., Roberts, R.M., Smith, M.F. and Youngquist, R.S.
 TITLE USDA Grant NRI-2002-03476: Bovine ESTs: Focus on Female Reproduction
 JOURNAL Unpublished (2002)
 COMMENT Contact: DNA Core Facility
 Animal Science - RS Prather
 University of Missouri-Columbia
 M616 Medical Sciences Bldg., Columbia, MO 65212, USA
 Tel: (573)882-0428
 Fax: (573)884-5552
 Email: bovine@net.missouri.edu
 POLYA=Yes.

FEATURES

Location/Qualifiers
 1..330
 /organism="Bos taurus"
 /mol_type="mRNA"
 /db_xref="taxon:9913"
 /clone_lib="bend"
 /note="Funding: The production of ESTs submitted in this project was funded by USDA Grant NRI-2002-03476 entitled 'Bovine ESTs: Focus on Female Reproduction' to RS Prather, E Antoniou, HA Garverick, JA Green, MC Lucy, RM Roberts, MF Smith and RS Youngquist. Genetic Source: Heifers for the project were purchased from Circle A Ranch, Iberia, MO (http://www.circlearanch.com/home.html). These heifers, while not registered have known Angus pedigrees going back at least 4 generations. Samples collected: The samples consisted of the following: germinal vesicle-stage oocytes; in vitro derived embryos (2-cell, morula, blastocyst and nuclear transfer blastocyst); in vivo blastocysts and conceptuses (days 8, 14, 16 and 18); corpora lutea (days 3, 5, 8, 14, 16, 18 and 35); ovarian follicles (days 0, non-recruited, recruited, early selected and preovulatory); oviduct (days 0, 3 and 5); endometrium (days 5, 8, 14, 16, 18 and 35); and placenta/embryo from day 35 conceptuses. Expanded descriptions of how the tissues were collected can be found at the following URL: http://genome.mnet.missouri.edu/Bovine/Methods.html. Library construction (Standard Protocol): All procedures have been described in detail elsewhere (Soares et al., 1994; Bonaldo et al., 1996; Jiang et al., 2001). Total cellular RNA from each sample was isolated by using STAT-60 reagent (Tel-Test, Friendswood, TX) and the poly(A)+ RNA was obtained by two rounds of purification with the Oligotex mRNA isolation kit (Qiagen) according to the manufacturer's instructions. The libraries were constructed by E. Ferguson and R. Woods essentially as described by the manufacturer's instructions provided with the SuperScript Plasmid System (Invitrogen, cat. no. 18248-013). Briefly, lmcg of poly(A)+ RNA was annealed at c37 degrees with 10mcg of NotI-tag-drt18 oligonucleotide (GCGTCGCGCGCG-tag-T18) and reverse transcribed at c37 degrees with SuperScript II (Invitrogen) reverse transcriptase (Jiang et al., 2001). The 'tag' represents a tissue/stage-specific ten-base sequence identifier (http://genome.uiowa.edu/pubsoft/software.html) present in the oligonucleotide used to prime first-strand synthesis.

Second strand synthesis was performed with T4 DNA polymerase in the presence of DNA ligase and RNase H. After second strand synthesis, the double-stranded cDNAs were ligated to SalI adapters (Invitrogen-Life Technologies) and digested with NotI. The cDNAs were size selected by passage through cDNA size fractionation columns (Invitrogen-Life Technologies). The cDNAs derived from each developmental stage of a particular tissue were mixed on an equimolar basis and ligated directionally into the NotI and SalI sites of the pCMV-SPORT6 vector (Invitrogen). After ligation of the inserts, the plasmids were electroporated into DH10B bacteria. Library Construction (PCR Protocol): The amount of mRNA that was recovered from oocytes and embryos was quite limiting and was not sufficient for library production with the standard protocol. Therefore, PCR-based protocol was utilized for producing libraries from sources in which the amount of extracted mRNA was small (oocytes and embryos). Poly-A RNA was isolated by using the MicroPoly(A) Pure kit from Ambion (cat. # 1918). The mRNA was reverse transcribed with a NotI-tag-drt18 oligonucleotide and a SMART oligonucleotide (Clontech) modified to contain a SalI site to generate full-length cDNA with a sequence complementary to the SMART oligonucleotide. Sequences within the SMART and dt oligonucleotides were used as primers to amplify the cDNAs by PCR with pfu turbo polymerase (Stratagene). The resulting PCR products were purified, digested with NotI and SalI and size fractionated by using Chroma Spin-1000 columns (Clontech). Purified cDNA from each PCR reaction was quantitated and mixed on an equimolar basis for ligation into the pCMV-SPORT6 vector. Preliminary Library Characterization: Randomly chosen clones from each library were analyzed by restriction digestion to determine average insert size (96 clones) and by sequencing (~4 96-well plates) to confirm library quality (e.g. the presence of short polyA+ tails, genomic DNA contamination (must be <1%), ribosomal RNA clones (must be <1%), etc.) and to provide a sequence database representing the predominant clones in each library. The clones were sequenced at the University of Missouri-Columbia DNA Core Facility. After production of the libraries, equal numbers of recombinants from each library were pooled to produce a single mixed library (mega-library) for more extensive sequencing. Bioinformatics work was performed by GK Springer's bioinformatics group (Spollen WG, Topinka CM, Khambati AA) in Computer Science at the University of Missouri-Columbia. Clone Requests: Requests for clones should be made to the Director of the University of Missouri DNA Core facility at: bovine@net.missouri.edu. Bonaldo MF, Lennon G, Soares MB. Normalization and Subtraction: Two approaches to facilitate gene discovery. Genome Res, 1996; 6:791-806. Jiang H, Bivens NJ, Ries JE, Whitworth KM, Green JA, Forrester LJ, Springer GK, Didion BA, Mathialagan N, Prather RS, Lucy MC (2001) Constructing cDNA libraries with fewer clones that contain long poly(da) tails. Biotechniques 31:38-42. Soares MB, MF Bonaldo, p Jelene, L Su, L Lawton, A Efstratiadis. 1994. Construction and characterization of a normalized cDNA library. Proc Natl Acad Sci, 91:9228-9232. TAG_TISSUP=Day 5 Uterus
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ORIGIN

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 Db 276 CCTCCTAGTTTGTAGGGATTGATCG 301
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RESULT 14
BE487585/c 331 bp mRNA linear EST 27-MAR-2003

LOCUS 176419 BARC 5BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION BE487585
VERSION BE487585.1 GI:9607118
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.

REFERENCE 1 (bases 1 to 331)
AUTHORS Sonstegard, T., Capuco, A.V., White, J., Van Tassell, C.P., Connor, E.E., Cho, J., Sultana, R., Shade, L., Wray, J.E., Wells, K.D. and Quackenbush, J.

TITLE Analysis of bovine mammary gland EST and functional annotation of the Bos taurus gene index

JOURNAL Mamm. Genome 13 (7), 373-379 (2002)
MEDLINE 22135956
PubMed 12140684

COMMENT Contact: Sonstegard TS
USDA, ARS, Beltsville Agricultural Research Center
Bldg. 200 Rm 2A, Beltsville, MD 20705, USA
Tel: 301 504 8416
Fax: 301 504 8414
Email: tadsepsi@ars.usda.gov

Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -mismatch 12 options.

PCR Primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCACAGTCACGACG
Plate: 138 row: M column: 9
Seq primer: ATTAGTGACACTATAG.

FEATURES
source Location/Qualifiers
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/lab_host="DH10B"
/clone_lib="BARC 5BOV"
/note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI; Library made from pooled mRNA isolated from mammary tissues at eight physiological, developmental, and disease states."

ORIGIN
Query Match 93.8%; Score 24.4; DB 2; Length 331;
Best Local Similarity 96.2%; Pred. No. 1.1;
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCTCCTAGTTTGTAGGGATTGATCG 26
|||||
Db 61 CCTCCTAGTTTGTGGGATTGATCG 36

RESULT 15
CN998120

LOCUS CN998120 331 bp mRNA linear EST 09-JUN-2004

DEFINITION UMC-bcl1 OA02-003-e08 Day 16 Corpus luteum from a pregnant animal
bcl1 Bos taurus cDNA 3', mRNA sequence.

ACCESSION CN998120
VERSION CN998120.1 GI:48490010
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.

REFERENCE 1 (bases 1 to 331)
AUTHORS Prather, R.S., Antoniou, E., Garverick, H.A., Green, J.A., Lucy, M.C.,

Roberts, R.M., Smith, M.F. and Youngquist, R.S.
USDA Grant NRI-2002-03476: Bovine ESTs: Focus on Female Reproduction
Unpublished (2002)
Contact: DNA Core Facility
Animal Science - RS Prather
University of Missouri-Columbia
M616 Medical Sciences Bldg., Columbia, MO 65212, USA
Tel: (573) 882-0428
Fax: (573) 884-5552
Email: bovine@net.missouri.edu
POLYA=Yes.

FEATURES
source Location/Qualifiers
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/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/clone_lib="bcl1"
/notes="Funding: The production of ESTs submitted in this project was funded by USDA Grant NRI-2002-03476 entitled 'Bovine ESTs: Focus on Female Reproduction' to RS Prather (Primary Investigator), E Antoniou, HA Garverick, JA Green, MC Lucy, RM Roberts, MF Smith and RS Youngquist. Genetic Source: Heifers for the project were purchased from Circle A Ranch, Iberia, MO (http://www.circlearanch.com/home.html). These heifers, while not registered have known Angus pedigrees going back at least 4 generations. Samples collected: The samples consisted of the following: germinal vesicle-stage oocytes; in vitro derived embryos (2-cell, morula, blastocyst and nuclear transfer blastocyst); in vivo corpora lutea (days 3, 5, 8, 14, 16, 18 and 35); ovarian follicles (days 0, non-recruited, recruited, early selected and preovulatory); oviduct (days 0, 3 and 5); endometrium (days 5, 8, 14, 16, 18 and 35); and placenta/embryo from day 35 conceptuses. Expanded descriptions of how the tissues were collected can be found at the following URL:
http://genome.mnnet.missouri.edu/Bovine/Methods.html. Library construction (Standard Protocol): All procedures have been described in detail elsewhere (Soares et al., 1994; Bonaldo et al., 1996; Jiang et al., 2001). Total cellular RNA from each sample was isolated by using STAT-60 reagent (Tel-Test, Friendswood, TX) and the poly(A)+ RNA was obtained by two rounds of purification with the Oligotex mRNA isolation kit (Qiagen) according to the manufacturer's instructions. The libraries were constructed essentially as described by the manufacturer's instructions provided with the SuperScript plasmid System (Invitrogen, cat. no. 18248-013). Briefly, 1mcg of poly(A)+ RNA was annealed at c37 degrees with 10mcg of NotI-tag-dT18 oligonucleotide (GCTGTCGCGCGC-tag-T18) and reverse transcribed at c37 degrees with SuperScript II (Invitrogen) reverse transcriptase (Jiang et al., 2001). The 'tag' represents a tissue/stage-specific ten-base sequence identifier (http://genome.ualowa.edu/pubsoft/software.html) present in the oligonucleotide used to prime first-strand synthesis. Second strand synthesis was performed with T4 DNA polymerase in the presence of DNA ligase and RNase H. After second strand synthesis, the double-stranded cDNAs were ligated to SalI adapters (Invitrogen-Life Technologies) and digested with NotI. The cDNAs were size selected by passage through cDNA size fractionation columns (Invitrogen-Life Technologies). The cDNAs derived from each developmental stage of a particular tissue were mixed on an equimolar basis and ligated directionally into the NotI and SalI sites of the pCMV-SPORT6 vector (Invitrogen). After ligation of the inserts, the plasmids were electroporated into DH10B bacteria. Library Construction (PCR Protocol): The amount of mRNA that was recovered from oocytes and embryos was quite limiting and

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 16, 2004, 23:47:45 ; Search time 38.7763 Seconds
(without alignments)
3621.431 Million cell updates/sec

Title: US-09-821-782E-2

Perfect score: 26

Sequence: 1 cctcctagttgttaggattgatcg 26

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3625171 seqs, 2700493622 residues

Total number of hits satisfying chosen parameters: 7250342

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

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- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq.*
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- 19: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
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- 21: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	24.4	93.8	200	9	US-09-960-352-9412
C 2	24.4	93.8	235	9	US-09-960-352-3962
C 3	24.4	93.8	241	9	US-09-960-352-5417
C 4	24.4	93.8	331	9	US-09-960-352-3998
C 5	24.4	93.8	411	9	US-09-960-352-12066
C 6	24.4	93.8	416	9	US-09-960-352-9213
C 7	24.4	93.8	417	9	US-09-960-352-13007
C 8	24.4	93.8	419	9	US-09-960-352-2332
C 9	24.4	93.8	448	9	US-09-960-352-8757
C 10	24.4	93.8	469	9	US-09-960-352-1158
C 11	24.4	93.8	475	9	US-09-960-352-5211
C 12	24.4	93.8	979	11	US-09-876-143-1164

C 13	22.8	87.7	120	16	US-10-242-535A-44171	Sequence 44171, A
C 14	22.8	87.7	120	16	US-10-085-783A-44171	Sequence 44171, A
C 15	22.8	87.7	231	9	US-09-878-178-824	Sequence 824, App
C 16	22.8	87.7	231	13	US-10-046-935-824	Sequence 824, App
C 17	22.8	87.7	231	14	US-10-146-502-824	Sequence 2469, Ap
C 18	22.8	87.7	308	14	US-10-066-543-2469	Sequence 2374, Ap
C 19	22.8	87.7	314	14	US-10-066-543-2374	Sequence 11785, A
C 20	22.8	87.7	317	16	US-10-242-535A-11785	Sequence 11785, A
C 21	22.8	87.7	317	16	US-10-085-783A-11785	Sequence 172, App
C 22	22.8	87.7	337	15	US-10-341-434-172	Sequence 36990, A
C 23	22.8	87.7	341	16	US-10-242-535A-36990	Sequence 2414, Ap
C 24	22.8	87.7	341	16	US-10-085-783A-36990	Sequence 2481, Ap
C 25	22.8	87.7	376	14	US-10-066-543-2414	Sequence 10725, A
C 26	22.8	87.7	376	14	US-10-066-543-2481	Sequence 10725, A
C 27	22.8	87.7	400	16	US-10-242-535A-10725	Sequence 1961, Ap
C 28	22.8	87.7	400	16	US-10-085-783A-10725	Sequence 5261, Ap
C 29	22.8	87.7	404	14	US-10-066-543-1961	Sequence 875, App
C 30	22.8	87.7	421	10	US-09-918-995-5261	Sequence 1324, Ap
C 31	22.8	87.7	433	14	US-10-060-036-875	Sequence 763, App
C 32	22.8	87.7	469	14	US-10-060-036-1324	Sequence 493, App
C 33	22.8	87.7	578	9	US-09-879-536-763	Sequence 562, App
C 34	22.8	87.7	591	10	US-09-871-161-493	Sequence 510, App
C 35	22.8	87.7	597	9	US-09-879-536-562	Sequence 812, App
C 36	22.8	87.7	619	10	US-09-871-161-510	Sequence 53, Appl
C 37	22.8	87.7	668	9	US-09-879-536-812	Sequence 38, Appl
C 38	22.8	87.7	793	18	US-10-484-364-53	Sequence 50, Appl
C 39	22.8	87.7	1004	18	US-10-484-364-38	Sequence 298, Appl
C 40	22.8	87.7	1082	15	US-10-139-794-50	Sequence 7, Appl
C 41	22.8	87.7	1107	10	US-09-822-846-298	Sequence 325, App
C 42	22.8	87.7	1140	15	US-10-325-881-7	Sequence 2047, Ap
C 43	22.8	87.7	1213	9	US-09-925-301-325	Sequence 208, App
C 44	22.8	87.7	1214	15	US-10-106-698-2047	
C 45	22.8	87.7	1955	15	US-10-170-385-208	

ALIGNMENTS

RESULT 1
US-09-960-352-9412/c
; Sequence 9412, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 9412
; LENGTH: 200
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 40-LIB34-065-Q1-E1-B12
US-09-960-352-9412

Query Match 93.8%; Score 24.4; DB 9; Length 200;
Best Local Similarity 96.2%; Pred. No. 0.2;
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 C C T C C T A G T T G T T A G G G A T T G A T C G 26
| | | | | | | | | | | | | | | | | | | | | | | | | |
Db 36 C C T C C T A G T T G T T G G G A T T G A T C G 11

RESULT 2
US-09-960-352-3962/c
; Sequence 3962, Application US/09960352
; Patent No. US20020137139A1

```
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; SEQ ID NO 3962
; LENGTH: 235
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 17-LIB34-051-Q1-E1-E1
US-09-960-352-3962

Query Match          93.8%; Score 24.4; DB 9; Length 235;
Best Local Similarity 96.2%; Pred. No. 0.21;
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCTCCTAGTTGTTAGGGATTGATCG 26
    |||||
Db 144 CCTCCTAGTTGTTAGGGATTGATCG 119
    |||||

RESULT 3
US-09-960-352-5417/c
; Sequence 5417, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; SEQ ID NO 5417
; LENGTH: 241
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 23-LIB34-052-Q1-E1-F3
US-09-960-352-5417

Query Match          93.8%; Score 24.4; DB 9; Length 241;
Best Local Similarity 96.2%; Pred. No. 0.21;
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCTCCTAGTTGTTAGGGATTGATCG 26
    |||||
Db 96 CCTCCTAGTTGTTAGGGATTGATCG 71
    |||||

RESULT 4
US-09-960-352-3998/c
; Sequence 3998, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; SEQ ID NO 3998
; LENGTH: 331
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 17-LIB34-084-Q1-E1-E9
US-09-960-352-3998

Query Match          93.8%; Score 24.4; DB 9; Length 331;
Best Local Similarity 96.2%; Pred. No. 0.22;
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCTCCTAGTTGTTAGGGATTGATCG 26
    |||||
Db 78 CCTCCTAGTTGTTAGGGATTGATCG 53
    |||||

RESULT 5
US-09-960-352-12066/c
; Sequence 12066, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 12066
; LENGTH: 411
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 52-BOVMS1-008-Q1-E1-E8
US-09-960-352-12066

Query Match          93.8%; Score 24.4; DB 9; Length 411;
Best Local Similarity 96.2%; Pred. No. 0.23;
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCTCCTAGTTGTTAGGGATTGATCG 26
    |||||
Db 135 CCTCCTAGTTGTTAGGGATTGATCG 110
    |||||

RESULT 6
US-09-960-352-9213/c
; Sequence 9213, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 9213
; LENGTH: 416
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 40-BOVMS1-002-Q1-E1-B8
US-09-960-352-9213

Query Match          93.8%; Score 24.4; DB 9; Length 416;
Best Local Similarity 96.2%; Pred. No. 0.23;
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 1 CCTCCTAGTTTGTAGGATTGATCG 26
Db 115 CCTCCTAGTTTGTGGGATTGATCG 90

RESULT 7
US-09-960-352-13007/c
; Sequence 13007, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 13007
; LENGTH: 417
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 56-BOVMS1-006-Q1-E1-F12
US-09-960-352-13007

Query Match 93.8%; Score 24.4; DB 9; Length 417;
Best Local Similarity 96.2%; Pred. No. 0.23;
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCTCCTAGTTTGTAGGATTGATCG 26
Db 152 CCTCCTAGTTTGTGGGATTGATCG 127

RESULT 8
US-09-960-352-2332/c
; Sequence 2332, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 2332
; LENGTH: 419
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 11-BOVMS1-005-Q1-E1-C3
US-09-960-352-2332

Query Match 93.8%; Score 24.4; DB 9; Length 419;
Best Local Similarity 96.2%; Pred. No. 0.23;
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCTCCTAGTTTGTAGGATTGATCG 26
Db 194 CCTCCTAGTTTGTGGGATTGATCG 169

RESULT 9
US-09-960-352-8757/c
; Sequence 8757, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 8757
; LENGTH: 448
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 38-BOVMS1-021-Q1-E1-B6
US-09-960-352-8757

Query Match 93.8%; Score 24.4; DB 9; Length 448;
Best Local Similarity 96.2%; Pred. No. 0.23;
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCTCCTAGTTTGTAGGATTGATCG 26
Db 404 CCTCCTAGTTTGTGGGATTGATCG 379

RESULT 10
US-09-960-352-1158/c
; Sequence 1158, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 1158
; LENGTH: 469
; TYPE: DNA
; ORGANISM: Bos taurus
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (422)
; OTHER INFORMATION: unsure at all n locations
; OTHER INFORMATION: Clone ID: 06-BOVMS1-014-Q1-E1-B5
US-09-960-352-1158

Query Match 93.8%; Score 24.4; DB 9; Length 469;
Best Local Similarity 96.2%; Pred. No. 0.23;
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCTCCTAGTTTGTAGGATTGATCG 26
Db 378 CCTCCTAGTTTGTGGGATTGATCG 353

RESULT 11
US-09-960-352-5211/c
; Sequence 5211, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
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; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 5211
; LENGTH: 475
; TYPE: DNA
; ORGANISM: Bos taurus
; NAME/KEY: unsure
; LOCATION: (7) (423)
; OTHER INFORMATION: unsure at all n locations
; OTHER INFORMATION: Clone ID: 23-BOVMS1-009-Q1-E1-F11
US-09-960-352-5211

Query Match 93.8%; Score 24.4; DB 9; Length 475;
Best Local Similarity 96.2%; Pred. No. 0.23;
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCTCCTAGTTTGTAGGATTGATCG 26
Db 379 CCTCCTAGTTTGTGGGATTGATCG 354
|||||

RESULT 12

US-09-876-143-1164/c
; Sequence 1164, Application US/09876143
; Publication No. US20040081958A1
; GENERAL INFORMATION:
; APPLICANT: Infogen Inc.
; APPLICANT: EILERTSEN, KENNETH J.
; APPLICANT: PFISTER-GENSKOW, MARTHA
; APPLICANT: CHILDS, LYNETTE
; APPLICANT: FORSYTHE, TODD
; APPLICANT: BISHOP, MICHAEL D.
; TITLE OF INVENTION: IDENTIFICATION AND USE OF MOLECULAR MARKERS INDICATING
; TITLE OF INVENTION: CELLULAR REPROGRAMMING
; FILE REFERENCE: 028040-0202
; CURRENT APPLICATION NUMBER: US/09/876,143
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 60/209,874
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 1744
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1164
; LENGTH: 979
; TYPE: DNA
; ORGANISM: Bovine
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(979)
; OTHER INFORMATION: n is a, c, g, or t
US-09-876-143-1164

Query Match 93.8%; Score 24.4; DB 11; Length 979;
Best Local Similarity 96.2%; Pred. No. 0.26;
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCTCCTAGTTTGTAGGATTGATCG 26
Db 192 CCTCCTAGTTTGTGGGATTGATCG 167
|||||

RESULT 13

US-10-242-535A-44171/c
; Sequence 44171, Application US/10242535A
; Publication No. US20040013663A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2005
; CURRENT APPLICATION NUMBER: US/10/242,535A
; CURRENT FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 10/085,783

; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 44171
; LENGTH: 120
; TYPE: DNA
; ORGANISM: Human
US-10-242-535A-44171

Query Match 87.7%; Score 22.8; DB 16; Length 120;
Best Local Similarity 92.3%; Pred. No. 1;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCTCCTAGTTTGTAGGATTGATCG 26
Db 59 CCTCCTAGTTTGTAGGACGATCG 34
|||||

RESULT 14

US-10-085-783A-44171/c
; Sequence 44171, Application US/10085783A
; Publication No. US20040037841A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2002
; CURRENT APPLICATION NUMBER: US/10/085,783A
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 44171
; LENGTH: 120
; TYPE: DNA
; ORGANISM: Human
US-10-085-783A-44171

Query Match 87.7%; Score 22.8; DB 15; Length 120;
Best Local Similarity 92.3%; Pred. No. 1;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCTCCTAGTTTGTAGGATTGATCG 26
Db 59 CCTCCTAGTTTGTAGGACGATCG 34
|||||

RESULT 15

US-09-878-178-824
; Sequence 824, Application US/09878178
; Patent No. US20020177552A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
; FILE REFERENCE: 210121.527
; CURRENT APPLICATION NUMBER: US/09/878,178
; CURRENT FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 2237
; SOFTWARE: FastSeq for Windows Version 4.0

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; SEQ ID NO 824
; LENGTH: 231
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(231)
; OTHER INFORMATION: n = A,T,C or G
US-09-878-178-824
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Query Match      87.7%; Score 22.8; DB 9; Length 231;
Best Local Similarity 92.3%; Pred. No. 1.1;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Qy      1 CCTCCTAGTTTGTAGGGATTGATCG 26
          |||||||
Db      199 CCTCCTAGTTTGTAGGGACGATCG 224
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Job time : 40.7763 secs
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OM nucleic - nucleic search, using sw model

Run on: November 16, 2004, 23:55:00 ; Search time 9.24665 Seconds
(without alignments)
1998.616 Million cell updates/sec

Title: US-09-821-782E-2

Perfect score: 26

Sequence: 1 cctcctagttttagggattgatcg 26

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

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- 2: /cgn2_6/ptodata/1/ina/5B COMB.seq.*
- 3: /cgn2_6/ptodata/1/ina/6A COMB.seq.*
- 4: /cgn2_6/ptodata/1/ina/6B COMB.seq.*
- 5: /cgn2_6/ptodata/1/ina/PCTUS COMB.seq.*
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	22.8	87.7	578	3	US-09-328-111-763
2	22.8	87.7	591	3	US-09-385-982-493
3	22.8	87.7	597	3	US-09-328-111-562
4	22.8	87.7	619	3	US-09-385-982-510
5	22.8	87.7	668	3	US-09-328-111-812
6	22.8	87.7	1140	4	US-09-377-497-7
7	22.8	87.7	16568	4	US-09-525-906-1
8	22.8	87.7	16569	3	US-09-097-889-2
9	22.8	87.7	16569	3	US-09-377-856-1
10	22.8	87.7	16569	4	US-09-302-681-2
11	22.8	87.7	16569	4	US-09-098-079-2
12	22.8	87.7	16569	4	US-10-053-611-1
13	21.2	81.5	30	1	US-08-647-584-46
14	21.2	81.5	602	3	US-09-385-982-375
15	20.8	80.0	315	4	US-09-313-294A-7516
16	18	69.2	99629	4	US-09-596-002-37
17	17.8	68.5	638	4	US-09-621-976-3609
18	17.6	67.7	616	4	US-09-270-767-31042
19	17.6	67.7	709	4	US-09-270-767-14799
20	17.2	66.2	12141	3	US-09-488-671-10
21	17	65.4	349	4	US-09-621-976-10857
22	17	65.4	447	4	US-09-107-532A-404
23	17	65.4	2242	4	US-09-738-946-9
24	16.8	64.6	21	1	US-08-647-584-107
25	16.6	63.8	472	4	US-09-513-999C-22922
26	16.6	63.8	618	3	US-09-385-982-200
27	16.6	63.8	720	1	US-08-153-848-35

Sequence 35, Appl
Sequence 35, Appl
Sequence 35, Appl
Sequence 12161, A
Sequence 1, Appl
Sequence 1, Appl
Sequence 5, Appl
Sequence 2479, Ap
Sequence 2493, Ap
Sequence 370, Ap
Sequence 3287, Ap
Sequence 3, Appl
Sequence 3, Appl
Sequence 3, Appl
Sequence 3, Appl
Sequence 3, Appl
Sequence 3, Appl
Sequence 3, Appl
Sequence 3, Appl

ALIGNMENTS

RESULT 1
US-09-328-111-763
; Sequence 763, Application US/09328111
; Patent No. 6262333
; GENERAL INFORMATION:
; APPLICANT: Endege, Wilson O.
; APPLICANT: Steinmann, Kathleen E.
; APPLICANT: Astle, Jon H.
; APPLICANT: Burgess, Christopher C.
; APPLICANT: Bushnell, Steven E.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Catino, Theodore J.
; APPLICANT: Derti, Adnan
; APPLICANT: Ford, Donna M.
; APPLICANT: Lewis, Marcia E.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
; FILE REFERENCE: CCD-257 (US)
; CURRENT APPLICATION NUMBER: US/09/328,111
; CURRENT FILING DATE: 1999-06-08
; EARLIER FILING DATE: 1998-06-10
; NUMBER OF SEQ ID NOS: 850
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 763
; LENGTH: 578
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(578)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-111-763

Query Match 87.7%; Score 22.8; DB 3; Length 578;
Best Local Similarity 92.3%; Pred. No. 0.054;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCTCCTAGTTTGTAGGATGATCG 26
|||
Db 305 CCTCCTAGTTTGTAGGACGATCG 330

RESULT 2
US-09-385-982-493
; Sequence 493, Application US/09385982
; Patent No. 6262334
; GENERAL INFORMATION:

; APPLICANT: ENDEGE, WILSON O., ET AL.
; TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
; FILE REFERENCE: CCNA-260XX
; CURRENT APPLICATION NUMBER: US/09/385,982
; CURRENT FILING DATE: 1999-08-30
; EARLIER APPLICATION NUMBER: 09/328,111
; EARLIER FILING DATE: 1999-06-08
; EARLIER APPLICATION NUMBER: 60/117,393
; EARLIER FILING DATE: 1999-01-27
; EARLIER APPLICATION NUMBER: 60/098,639
; EARLIER FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 544
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 493
; LENGTH: 591
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(591)
; OTHER INFORMATION: n = A,T,C or G
US-09-385-982-493

Query Match 87.7%; Score 22.8; DB 3; Length 591;
Best Local Similarity 92.3%; Pred. No. 0.054;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCTCTAGTTTCTTAGGATTCATCG 26
Db 199 CCTCTAGTTTCTTAGGACGGATCG 224

RESULT 3

US-09-328-111-562
; Sequence 562, Application US/09328111
; Patent No. 6262333

; GENERAL INFORMATION:
; APPLICANT: Endege, Wilson O.
; APPLICANT: Steinmann, Kathleen E.
; APPLICANT: Astle, Jon H.
; APPLICANT: Burgess, Christopher C.
; APPLICANT: Bushnell, Steven E.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Catino, Theodore J.
; APPLICANT: Derti, Adnan
; APPLICANT: Ford, Donna M.
; APPLICANT: Lewis, Marcia E.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
; FILE REFERENCE: CCD-257 (US)
; CURRENT APPLICATION NUMBER: US/09/328,111
; CURRENT FILING DATE: 1999-06-08
; EARLIER APPLICATION NUMBER: US 60/088,801
; EARLIER FILING DATE: 1998-06-10
; NUMBER OF SEQ ID NOS: 850
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 562
; LENGTH: 597
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(597)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-111-562

Query Match 87.7%; Score 22.8; DB 3; Length 597;
Best Local Similarity 92.3%; Pred. No. 0.054;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCTCTAGTTTCTTAGGATTCATCG 26
Db 205 CCTCTAGTTTCTTAGGACGGATCG 230

RESULT 4

US-09-385-982-510
; Sequence 510, Application US/09385982
; Patent No. 6262334
; GENERAL INFORMATION:
; APPLICANT: ENDEGE, WILSON O., ET AL.
; TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
; FILE REFERENCE: CCNA-260XX
; CURRENT APPLICATION NUMBER: US/09/385,982
; CURRENT FILING DATE: 1999-08-30
; EARLIER APPLICATION NUMBER: 09/328,111
; EARLIER FILING DATE: 1999-06-08
; EARLIER APPLICATION NUMBER: 60/117,393
; EARLIER FILING DATE: 1999-01-27
; EARLIER APPLICATION NUMBER: 60/098,639
; EARLIER FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 544
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 510
; LENGTH: 619
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(619)
; OTHER INFORMATION: n = A,T,C or G
US-09-385-982-510

Query Match 87.7%; Score 22.8; DB 3; Length 619;
Best Local Similarity 92.3%; Pred. No. 0.054;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCTCTAGTTTCTTAGGATTCATCG 26
Db 199 CCTCTAGTTTCTTAGGACGGATCG 224

RESULT 5

US-09-328-111-812
; Sequence 812, Application US/09328111
; Patent No. 6262333
; GENERAL INFORMATION:
; APPLICANT: Endege, Wilson O.
; APPLICANT: Steinmann, Kathleen E.
; APPLICANT: Astle, Jon H.
; APPLICANT: Burgess, Christopher C.
; APPLICANT: Bushnell, Steven E.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Catino, Theodore J.
; APPLICANT: Derti, Adnan
; APPLICANT: Ford, Donna M.
; APPLICANT: Lewis, Marcia E.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
; FILE REFERENCE: CCD-257 (US)
; CURRENT APPLICATION NUMBER: US/09/328,111
; CURRENT FILING DATE: 1999-06-08
; EARLIER APPLICATION NUMBER: US 60/088,801
; EARLIER FILING DATE: 1998-06-10
; NUMBER OF SEQ ID NOS: 850
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 812
; LENGTH: 668
; TYPE: DNA
; ORGANISM: Homo sapiens

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; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(668)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-111-812

Query Match      87.7%; Score 22.8; DB 3; Length 668;
Best Local Similarity 92.3%; Pred. No. 0.055; 2; Indels 0; Gaps 0;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTCCTAGTTTCTTAGGGATTGATCG 26
   |||||
Db 199 CCTCCTAGTTTCTTAGGGACGGATCG 224
   |||||

RESULT 6
US-09-377-497-7/c
; Sequence 7, Application US/09377497
; Patent No. 6670119
; GENERAL INFORMATION:
; APPLICANT: YOSHIKAWA, YOSHIE
; APPLICANT: MUKAI, HIROYUKI
; APPLICANT: ASADA, KIYOZO
; APPLICANT: HINO, FUMITSUGU
; APPLICANT: KATO, IKUNOSHIN
; TITLE OF INVENTION: CANCER-ASSOCIATED GENES
; FILE REFERENCE: 1422-388P
; CURRENT APPLICATION NUMBER: US/09/377,497
; CURRENT FILING DATE: 1999-08-20
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 1140
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: any n or Xaa = unknown
US-09-377-497-7

Query Match      87.7%; Score 22.8; DB 4; Length 1140;
Best Local Similarity 92.3%; Pred. No. 0.061; 2; Indels 0; Gaps 0;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCCTAGTTTCTTAGGGATTGATCG 26
   |||||
Db 869 CCTCCTAGTTTCTTAGGGACGGATCG 844
   |||||

RESULT 7
US-09-525-906-1/c
; Sequence 1, Application US/09525906
; Patent No. 6605433
; GENERAL INFORMATION:
; APPLICANT: Jen, Jen
; APPLICANT: Sidransky, David
; APPLICANT: Kinzler, Kenneth
; APPLICANT: Vogelstein, Bert
; APPLICANT: Fliss, Makiko
; APPLICANT: Polyak, Kornelia
; TITLE OF INVENTION: Mitochondrial Dosimeter
; FILE REFERENCE: 1107.85815
; CURRENT APPLICATION NUMBER: US/09/525,906
; CURRENT FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: 09/377,856
; PRIOR FILING DATE: 1999-08-20
; PRIOR APPLICATION NUMBER: 60/097,307
; PRIOR FILING DATE: 1998-08-20
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 16568
; TYPE: DNA
; ORGANISM: Homo sapiens
```

```
US-09-525-906-1

Query Match      87.7%; Score 22.8; DB 4; Length 16568;
Best Local Similarity 92.3%; Pred. No. 0.1; 2; Indels 0; Gaps 0;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTCCTAGTTTCTTAGGGATTGATCG 26
   |||||
Db 15614 CCTCCTAGTTTCTTAGGGACGGATCG 15589
   |||||

RESULT 8
US-09-097-889-2/c
; Sequence 2, Application US/09097889
; Patent No. 6218117
; GENERAL INFORMATION:
; APPLICANT: Herrnstadt, Corrina
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Davis, Robert E.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING
; TITLE OF INVENTION: AGENTS THAT QUANTITATIVELY ALTER DETECTABLE
; TITLE OF INVENTION: EXTRAMITOCHONDRIAL DNA: MITOCHONDRIAL DNA RATIOS
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/097,889
; FILING DATE: 15-JUN-1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Rosenman Ph.D., Stephen J.
; REGISTRATION NUMBER: 43,058
; REFERENCE/DOCKET NUMBER: 660088.417
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16569 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-097-889-2

Query Match      87.7%; Score 22.8; DB 3; Length 16569;
Best Local Similarity 92.3%; Pred. No. 0.1; 2; Indels 0; Gaps 0;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTCCTAGTTTCTTAGGGATTGATCG 26
   |||||
Db 15615 CCTCCTAGTTTCTTAGGGACGGATCG 15590
   |||||

RESULT 9
US-09-377-856-1/c
; Sequence 1, Application US/09377856
; Patent No. 6344322
; GENERAL INFORMATION:
; APPLICANT: Polyak, Kornelia
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; TITLE OF INVENTION: Subtle Mitochondrial Mutations as Tumor
; TITLE OF INVENTION: Markers
```

```
; FILE REFERENCE: 1107.82346
; CURRENT APPLICATION NUMBER: US/09/377,856
; PRIOR FILING DATE: 1999-08-20
; PRIOR APPLICATION NUMBER: 60/097,307
; PRIOR FILING DATE: 1998-08-20
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 16569
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-377-856-1

Query Match      87.7%; Score 22.8; DB 3; Length 16569;
Best Local Similarity 92.3%; Pred. No. 0.1;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCTCCTAGTTTGTAGGAGTTCG 26
Db 15615 CCTCCTAGTTTGTAGGAGTTCG 15590

RESULT 10
US-09-302-681-2/c
; Sequence 2, Application US/09302681
; Patent No. 6441149
; GENERAL INFORMATION:
; APPLICANT: Herrnstadt, Corrina
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Clevenger, William
; APPLICANT: Fahy, Eoin F.
; APPLICANT: Davis, Robert E.
; TITLE OF INVENTION: DIAGNOSTIC METHOD BASED ON
; FILE REFERENCE: 660088.416C1
; CURRENT APPLICATION NUMBER: US/09/302,681
; CURRENT FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 16569
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-302-681-2

Query Match      87.7%; Score 22.8; DB 4; Length 16569;
Best Local Similarity 92.3%; Pred. No. 0.1;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCTCCTAGTTTGTAGGAGTTCG 26
Db 15615 CCTCCTAGTTTGTAGGAGTTCG 15590

RESULT 11
US-09-098-079-2/c
; Sequence 2, Application US/09098079
; Patent No. 6489095
; GENERAL INFORMATION:
; APPLICANT: Herrnstadt, Corrina
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Clevenger, William
; APPLICANT: Fahy, Eoin F.
; APPLICANT: Davis, Robert E.
; TITLE OF INVENTION: DIAGNOSTIC METHOD BASED ON QUANTIFICATION OF
; FILE REFERENCE: 660088.416C1
; CURRENT APPLICATION NUMBER: US/09/302,681
; CURRENT FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 16569
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-302-681-2

Query Match      87.7%; Score 22.8; DB 4; Length 16569;
Best Local Similarity 92.3%; Pred. No. 0.1;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCTCCTAGTTTGTAGGAGTTCG 26
Db 15615 CCTCCTAGTTTGTAGGAGTTCG 15590

RESULT 12
US-10-053-611-1/c
; Sequence 1, Application US/10053611
; Patent No. 6750021
; GENERAL INFORMATION:
; APPLICANT: Polyak, Kornelia
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; TITLE OF INVENTION: Subtle Mitochondrial Mutations as Tumor
; FILE REFERENCE: 1107.82346
; CURRENT APPLICATION NUMBER: US/10/053,611
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: US/09/377,856
; PRIOR FILING DATE: 1999-08-20
; PRIOR APPLICATION NUMBER: 60/097,307
; PRIOR FILING DATE: 1998-08-20
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 16569
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-053-611-1

Query Match      87.7%; Score 22.8; DB 4; Length 16569;
Best Local Similarity 92.3%; Pred. No. 0.1;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCTCCTAGTTTGTAGGAGTTCG 26
Db 15615 CCTCCTAGTTTGTAGGAGTTCG 15590

RESULT 13
US-08-647-584-46/c
; Sequence 46, Application US/08647584
; Patent No. 5786144
; GENERAL INFORMATION:
```

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; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/098,079
; FILING DATE: 15-JUN-1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Rosenman Ph.D., Stephen J.
; REGISTRATION NUMBER: 43,058
; REFERENCE/DOCKET NUMBER: 660088.416
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16569 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-098-079-2

Query Match      87.7%; Score 22.8; DB 4; Length 16569;
Best Local Similarity 92.3%; Pred. No. 0.1;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCTCCTAGTTTGTAGGAGTTCG 26
Db 15615 CCTCCTAGTTTGTAGGAGTTCG 15590

RESULT 12
US-10-053-611-1/c
; Sequence 1, Application US/10053611
; Patent No. 6750021
; GENERAL INFORMATION:
; APPLICANT: Polyak, Kornelia
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; TITLE OF INVENTION: Subtle Mitochondrial Mutations as Tumor
; FILE REFERENCE: 1107.82346
; CURRENT APPLICATION NUMBER: US/10/053,611
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: US/09/377,856
; PRIOR FILING DATE: 1999-08-20
; PRIOR APPLICATION NUMBER: 60/097,307
; PRIOR FILING DATE: 1998-08-20
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 16569
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-053-611-1

Query Match      87.7%; Score 22.8; DB 4; Length 16569;
Best Local Similarity 92.3%; Pred. No. 0.1;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCTCCTAGTTTGTAGGAGTTCG 26
Db 15615 CCTCCTAGTTTGTAGGAGTTCG 15590

RESULT 13
US-08-647-584-46/c
; Sequence 46, Application US/08647584
; Patent No. 5786144
; GENERAL INFORMATION:
```


APPLICANT: De Salle, Rob
APPLICANT: Birstein, Vadim J.
TITLE OF INVENTION: METHOD AND COMPOSITIONS FOR
IDENTIFICATION OF SPECIES ORIGIN OF CAVIAR
NUMBER OF SEQUENCES: 145
CORRESPONDENCE ADDRESS:
ADDRESSEE: Weil, Gotshal & Manges LLP
STREET: 2882 Sand Hill Road, Suite 280
CITY: Menlo Park
STATE: California
COUNTRY: U.S.A.
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/647,584
FILING DATE: 13-MAY-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Baran, Alexandra J.
REGISTRATION NUMBER: 39,101
REFERENCE/DOCKET NUMBER: 14503.4010
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 926-6200
TELEFAX: (415) 854-3713
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-647-584-46

Query Match 81.5%; Score 21.2; DB 1; Length 30;
Best Local Similarity 88.5%; Pred. No. 0.19;
Matches 23; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCTCCTAGTTTGTAGGGATTGATCG 26
Db 26 CCGCCTAGTTTGTAGGGATTGATCG 1

RESULT 14

US-09-385-982-375
Sequence 375, Application US/09385982
Patent No. 6262334
GENERAL INFORMATION:
APPLICANT: ENDEGE, WILSON O., ET AL.
TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
FILE REFERENCE: CCDA-260XX
CURRENT APPLICATION NUMBER: US/09/385,982
CURRENT FILING DATE: 1999-08-30
EARLIER APPLICATION NUMBER: 09/328,111
EARLIER FILING DATE: 1999-06-08
EARLIER APPLICATION NUMBER: 60/117,393
EARLIER FILING DATE: 1999-01-27
EARLIER APPLICATION NUMBER: 60/098,639
EARLIER FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 544
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 375
LENGTH: 602
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)-(602)
OTHER INFORMATION: n = A,T,C or G

US-09-385-982-375

Query Match 81.5%; Score 21.2; DB 3; Length 602;
Best Local Similarity 88.5%; Pred. No. 0.33;
Matches 23; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCTCCTAGTTTGTAGGGATTGATCG 26
Db 199 CCTCCTAGTTTGTAGGGACGGATCG 224

RESULT 15

US-09-313-294A-7516/c
Sequence 7516, Application US/09313294A
Patent No. 6476212
GENERAL INFORMATION:
APPLICANT: Lalgudi, Raghunath V.
APPLICANT: Ito, Laura Y.
APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
FILE REFERENCE: PL-0017 US
CURRENT APPLICATION NUMBER: US/09/313,294A
CURRENT FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 7600
SOFTWARE: PERL Program
SEQ ID NO 7516
LENGTH: 315
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. 6476212 700381866H1
NAME/KEY: unsure
LOCATION: 32, 56, 84, 87, 117-118, 160, 196, 244
OTHER INFORMATION: a, t, c, g, or other
US-09-313-294A-7516

Query Match 80.0%; Score 20.8; DB 4; Length 315;
Best Local Similarity 84.6%; Pred. No. 0.46;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CCTCCTAGTTTGTAGGGATTGATCG 26
Db 119 CCCCCTAGTTTGTAGGGACGGATCG 94

Search completed: November 17, 2004, 03:15:11
Job time : 11.2467 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 16, 2004, 16:25:24 ; Search time 40.7744 Seconds
(without alignments)
3218.578 Million cell updates/sec

Title: US-09-821-782E-1

Perfect score: 25

Sequence: 1 taccatgaggacaataatcattctg 25

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_23Sep04:*

- 1: geneseqn1980s:*
- 2: geneseqn1990s:*
- 3: geneseqn2000s:*
- 4: geneseqn2001as:*
- 5: geneseqn2001bs:*
- 6: geneseqn2002as:*
- 7: geneseqn2002bs:*
- 8: geneseqn2003as:*
- 9: geneseqn2003bs:*
- 10: geneseqn2003cs:*
- 11: geneseqn2003ds:*
- 12: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25	100.0	25	8	ABQ83297 Cytochrom
2	25	100.0	329	8	ABX49123 Bovine ES
3	25	100.0	346	8	ABX41392 Bovine ES
4	25	100.0	353	8	ABX41185 Bovine ES
5	25	100.0	380	8	ABX42082 Bovine ES
6	25	100.0	388	8	ABX36231 Bovine ES
7	25	100.0	397	8	ABX42640 Bovine ES
8	25	100.0	402	8	ABX47053 Bovine ES
9	25	100.0	409	8	ABX44209 Bovine ES
10	25	100.0	409	8	ABX42249 Bovine ES
11	25	100.0	409	8	ABX39507 Bovine ES
12	25	100.0	411	8	ABX43333 Bovine ES
13	25	100.0	412	8	ABX35955 Bovine ES
14	25	100.0	413	8	ABX37092 Bovine ES
15	25	100.0	414	8	ABX46099 Bovine ES
16	25	100.0	415	8	ABX40021 Bovine ES
17	25	100.0	417	8	ABX41849 Bovine ES
18	25	100.0	417	8	ABX45538 Bovine ES
19	25	100.0	419	8	ABX37811 Bovine ES
20	25	100.0	420	8	ABX44580 Bovine ES
21	25	100.0	420	8	ABX35249 Bovine ES

22	25	100.0	421	8	ABX39415	Abx39415 Bovine ES
23	25	100.0	422	8	ABX47816	Abx47816 Bovine ES
24	25	100.0	424	8	ABX39981	Abx39981 Bovine ES
25	25	100.0	425	8	ABX44677	Abx44677 Bovine ES
26	25	100.0	428	8	ABX40056	Abx40056 Bovine ES
27	25	100.0	429	8	ABX46840	Abx46840 Bovine ES
28	25	100.0	432	8	ABX42116	Abx42116 Bovine ES
29	25	100.0	433	8	ABX47629	Abx47629 Bovine ES
30	25	100.0	435	8	ABX44491	Abx44491 Bovine ES
31	25	100.0	436	8	ABX36609	Abx36609 Bovine ES
32	25	100.0	443	8	ABX43069	Abx43069 Bovine ES
33	25	100.0	444	8	ABX40780	Abx40780 Bovine ES
34	25	100.0	445	8	ABX44982	Abx44982 Bovine ES
35	25	100.0	446	8	ABX47632	Abx47632 Bovine ES
36	25	100.0	446	8	ABX48097	Abx48097 Bovine ES
37	25	100.0	447	8	ABX39586	Abx39586 Bovine ES
38	25	100.0	447	8	ABX38849	Abx38849 Bovine ES
39	25	100.0	448	8	ABX37805	Abx37805 Bovine ES
40	25	100.0	455	8	ABX38792	Abx38792 Bovine ES
41	25	100.0	458	8	ABX38588	Abx38588 Bovine ES
42	25	100.0	472	8	ABQ83339	Abq83339 Mitochond
43	25	100.0	472	8	ABQ83321	Abq83321 Mitochond
44	25	100.0	472	8	ABQ83322	Abq83322 Mitochond
45	25	100.0	472	8	ABQ83332	Abq83332 Mitochond

ALIGNMENTS

RESULT 1
ABQ83297
ID ABQ83297 standard; DNA; 25 BP.
XX
AC ABQ83297;
XX
DT 18-JAN-2003 (first entry)
XX
DE Cytochrome b gene universal PCR primer mcb 398 SEQ ID NO:2.
XX
KW Mitochondrial cytochrome b gene; mitochondrial; cytochrome b;
KW identification; criminal investigation; animal poaching; PCR primer; ss.
XX
OS Synthetic.
XX
PN WO200272728-A1.
XX
PD 03-OCT-2002.
XX
PF 28-MAR-2001; 2001WO-IN000055.
XX
PR 28-MAR-2001; 2001WO-IN000055.
XX
PA (COUL) COUNCIL SCI & IND RES.
XX
PI Verma SK, Singh L;
XX
DR WPI; 2003-018945/01.
XX
PT New universal primers, mcb 398 and mcb 869, capable of amplifying a
PT fragment of cytochrome b gene of any animal species, useful for
PT establishing the identity of biological materials and animals for
PT molecular evidence in forensics.
XX
PS Claim 1; Page 116; 128pp; English.
XX
CC The present invention describes universal primers, mcb 398 and mcb 869
CC (see ABQ83297 and ABQ83298), capable of amplifying a fragment of
CC cytochrome b gene of any animal species in polymerase chain reaction
CC (PCR) and revealing the identity of the biological material of any animal
CC of unknown origin at species and sub-species level. Also described is a
CC method for the identification of the animal from a biological sample. The
CC method is used for animal identification to establish the crime with the
CC criminal beyond a reasonable doubt, to establish the identity of

biological materials such as skin, horns confiscated from animal poachers, if it is that of an endangered species, for the purpose of molecular evidence of animal hunting and related crime in the court of law, so that human violation of the wildlife resources could be controlled, to have an idea of the geographical location of the committed of wildlife crime based on the cytochrome b gene haplotype of poached animal identified by the universal primer invented, to detect the adulteration of animal meat in food products for the purpose of food fortification, by the food fortification agencies, to provide a universal technique for detection of the origin of blood or blood stains collected from the scene of the crime related to offenses such as murder and rape, in order to establish the origin of blood found at the scene of the crime when it sounds as if criminals intentionally spread the blood of an animal at the scene of the crime to confuse the crime investigators and forensic scientists with human blood, and so that the method can be converted to a commercial molecular kit and DNA chips based applications for wildlife identification in forensics

Sequence 25 BP; 9 A; 5 C; 4 G; 7 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.21; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TACCATGAGGACAAATATCATCTG 25

DB 1 TACCATGAGGACAAATATCATCTG 25

RESULT 2

ABX49123

ID ABX49123 standard; cDNA; 329 BP.

XX AC ABX49123;

XX DT 21-FEB-2003 (first entry)

XX DE Bovine EST associated with lactation/muscle/fat deposition #14288.

XX KW Bovine; ss; EST; expressed sequence tag; lactation; LMFD;
XX KW muscle deposition; fat deposition; genome mapping; gene identification;
XX KW gene analysis; cattle breeding.

XX OS Bos Taurus.

XX PN US2002137139-A1.

XX PD 26-SEP-2002.

XX PF 24-SEP-2001; 2001US-00960352.

XX PR 12-JAN-1999; 99US-0115707P.

XX PR 11-JAN-2000; 2000US-00480902.

XX PA (BYAT/) BYATT J C.

XX PA (MATH/) MATHIALAGAN N.

XX PA (TAON/) TAO N.

XX PA (WARR/) WARREN W C.

XX PI Byatt JC, Mathialagan N, Tao N, Warren WC;

XX DR WPI; 2003-110599/10.

XX PT New nucleic acid associated with lactation, and muscle and fat
XX PT deposition, useful for genome mapping, gene identification and analysis,
XX PT cattle breeding, or for genetically improving cattle.

XX PS Claim 2; SEQ ID NO 14288; 245pp; English.

XX CC The invention relates to a purified nucleic acid molecule associated with
XX CC lactation or muscle and fat deposition (designated LMFD), derived from
XX CC cattle, and the LMFD nucleic acid can specifically hybridise to a second
XX CC nucleic acid molecule comprising any of 15112 nucleotide sequences,

CC appearing as ABX34836-ABX49947, or complements of them. Also included are
CC (1) a transformed cell having a nucleic acid comprising an LMFD nucleic
CC acid linked to a promoter and a 3' non-translated sequence that
CC functions in the cell to cause termination of transcription and addition
CC of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and
CC (2) determining a level or pattern of a molecule in a bovine cell or
CC tissue comprising: (a) incubating a marker nucleic acid (comprising any
CC of the 15112 nucleic acid sequences or its complement or fragment) with a
CC complementary nucleic acid molecule obtained from the bovine cell or
CC tissue, where hybridisation between the marker nucleic acid and the
CC complementary nucleic acid permits the detection of the molecule; and (b)
CC detecting the level or pattern of the complementary nucleic acid, where
CC the detection of the complementary nucleic acid is predictive of the
CC level or pattern of the molecule. The LMFD nucleic acid is used for
CC determining a level or pattern of a molecule in a bovine cell or tissue.
CC It is useful for genome mapping, gene identification and analysis, cattle
CC breeding, preparation of constructs for use in cattle gene expression, or
CC for genetically improving cattle. The present sequence is one of the
CC 15112 bovine LMFD EST (expressed sequence tag) nucleic acids. Note: The
CC present sequence was not shown in the specification but was obtained in
CC electronic format from the USPTO web site:

CC seqdata.uspto.gov/sequence.html?DocID=20020137139

XX SQ Sequence 329 BP; 96 A; 78 C; 66 G; 89 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 8; Length 329;

Best Local Similarity 100.0%; Pred. No. 0.26; Length 329;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TACCATGAGGACAAATATCATCTG 25

DB 305 TACCATGAGGACAAATATCATCTG 329

RESULT 3

ABX41392

ID ABX41392 standard; cDNA; 346 BP.

XX AC ABX41392;

XX DT 20-FEB-2003 (first entry)

XX DE Bovine EST associated with lactation/muscle/fat deposition #6557.

XX KW Bovine; ss; EST; expressed sequence tag; lactation; LMFD;
XX KW muscle deposition; fat deposition; genome mapping; gene identification;
XX KW gene analysis; cattle breeding.

XX OS Bos Taurus.

XX PN US2002137139-A1.

XX PD 26-SEP-2002.

XX PF 24-SEP-2001; 2001US-00960352.

XX PR 12-JAN-1999; 99US-0115707P.

XX PR 11-JAN-2000; 2000US-00480902.

XX PA (BYAT/) BYATT J C.

XX PA (MATH/) MATHIALAGAN N.

XX PA (TAON/) TAO N.

XX PA (WARR/) WARREN W C.

XX PI Byatt JC, Mathialagan N, Tao N, Warren WC;

XX DR WPI; 2003-110599/10.

XX PT New nucleic acid associated with lactation, and muscle and fat

XX PT deposition, useful for genome mapping, gene identification and analysis,

XX PT cattle breeding, or for genetically improving cattle.

XX PS Claim 2; SEQ ID NO 6557; 245pp; English.

XX The invention relates to a purified nucleic acid molecule associated with
 CC lactation or muscle and fat deposition (designated LMFD), derived from
 CC cattle, and the LMFD nucleic acid can specifically hybridize to a second
 CC nucleic acid molecule comprising any of 15112 nucleotide sequences,
 CC appearing as ABX34836-ABX49947, or complements of them. Also included are
 CC ; (1) a transformed cell having a nucleic acid comprising an LMFD nucleic
 CC acid linked to a promoter and a 3' non- translated sequence that
 CC functions in the cell to cause termination of transcription and addition
 CC of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and
 CC (2) determining a level or pattern of a molecule in a bovine cell or
 CC tissue comprising: (a) incubating a marker nucleic acid (comprising any
 CC of the 15112 nucleic acid sequences or its complement or fragment) with a
 CC complementary nucleic acid molecule obtained from the bovine cell or
 CC tissue, where hybridisation between the marker nucleic acid and the
 CC complementary nucleic acid permits the detection of the molecule; and (b)
 CC detecting the level or pattern of the complementary nucleic acid, where
 CC the detection of the complementary nucleic acid is predictive of the
 CC level or pattern of the molecule. The LMFD nucleic acid is used for
 CC determining a level or pattern of a molecule in a bovine cell or tissue.
 CC It is useful for genome mapping, gene identification and analysis, cattle
 CC breeding, preparation of constructs for use in cattle gene expression, or
 CC for genetically improving cattle. The present sequence is one of the
 CC 15112 bovine LMFD EST (expressed sequence tag) nucleic acids. Note: The
 CC present sequence was not shown in the specification but was obtained in
 CC electronic format from the USPTO web site:
 CC seqdata.uspto.gov/sequence.html?docID=20020137139

XX Sequence 346 BP; 106 A; 82 C; 55 G; 103 T; 0 U; 0 Other;
 Query Match 100.0%; Score 25; DB 8; Length 346;
 Best Local Similarity 100.0%; Pred. No. 0.27;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TACCATGAGGACAAATATCATCTG 25
 ||||||||||||||||||||
 Db 174 TACCATGAGGACAAATATCATCTG 198

RESULT 4
 ABX41185
 ID ABX41185 standard; cDNA; 353 BP.
 XX
 AC ABX41185;
 XX
 XX
 XX
 XX 20-FEB-2003 (first entry)
 XX
 DE Bovine EST associated with lactation/muscle/fat deposition #6350.
 XX
 KW Bovine; ss; EST; expressed sequence tag; lactation; LMFD;
 KW muscle deposition; fat deposition; genome mapping; gene identification;
 KW gene analysis; cattle breeding.
 XX
 XX Bos Taurus.
 OS

XX US2002137139-A1.
 XX
 XX 26-SEP-2002.
 XX
 XX 24-SEP-2001; 2001US-00960352.
 XX
 XX 12-JAN-1999; 99US-0115707P.
 XX 11-JAN-2000; 2000US-00480902.
 XX
 XX (BYAT//) BYATT J C.
 XX (MATH//) MATHIALAGAN N.
 XX (TAON//) TAO N.
 XX (WARR//) WARREN W C.
 XX
 XX Byatt JC, Mathialagan N, Tao N, Warren WC;
 XX WPI; 2003-110599/10.
 XX

PT New nucleic acid associated with lactation, and muscle and fat
 PT deposition, useful for genome mapping, gene identification and analysis,
 PT cattle breeding, or for genetically improving cattle.
 XX

XX Claim 2; SEQ ID NO 6350; 245pp; English.

XX The invention relates to a purified nucleic acid molecule associated with
 CC lactation or muscle and fat deposition (designated LMFD), derived from
 CC cattle, and the LMFD nucleic acid can specifically hybridize to a second
 CC nucleic acid molecule comprising any of 15112 nucleotide sequences,
 CC appearing as ABX34836-ABX49947, or complements of them. Also included are
 CC ; (1) a transformed cell having a nucleic acid comprising an LMFD nucleic
 CC acid linked to a promoter and a 3' non- translated sequence that
 CC functions in the cell to cause termination of transcription and addition
 CC of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and
 CC (2) determining a level or pattern of a molecule in a bovine cell or
 CC tissue comprising: (a) incubating a marker nucleic acid (comprising any
 CC of the 15112 nucleic acid sequences or its complement or fragment) with a
 CC complementary nucleic acid molecule obtained from the bovine cell or
 CC tissue, where hybridisation between the marker nucleic acid and the
 CC complementary nucleic acid permits the detection of the molecule; and (b)
 CC detecting the level or pattern of the complementary nucleic acid, where
 CC the detection of the complementary nucleic acid is predictive of the
 CC level or pattern of the molecule. The LMFD nucleic acid is used for
 CC determining a level or pattern of a molecule in a bovine cell or tissue.
 CC It is useful for genome mapping, gene identification and analysis, cattle
 CC breeding, preparation of constructs for use in cattle gene expression, or
 CC for genetically improving cattle. The present sequence is one of the
 CC 15112 bovine LMFD EST (expressed sequence tag) nucleic acids. Note: The
 CC present sequence was not shown in the specification but was obtained in
 CC electronic format from the USPTO web site:
 CC seqdata.uspto.gov/sequence.html?docID=20020137139

XX Sequence 353 BP; 106 A; 91 C; 56 G; 100 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 8; Length 353;
 Best Local Similarity 100.0%; Pred. No. 0.27;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TACCATGAGGACAAATATCATCTG 25
 ||||||||||||||||||||
 Db 324 TACCATGAGGACAAATATCATCTG 348

RESULT 5
 ABX42082
 ID ABX42082 standard; cDNA; 380 BP.
 XX
 AC ABX42082;
 XX
 XX
 XX 20-FEB-2003 (first entry)
 XX
 DE Bovine EST associated with lactation/muscle/fat deposition #7247.
 XX
 KW Bovine; ss; EST; expressed sequence tag; lactation; LMFD;
 KW muscle deposition; fat deposition; genome mapping; gene identification;
 KW gene analysis; cattle breeding.
 XX
 XX Bos Taurus.
 OS

XX US2002137139-A1.
 XX
 XX 26-SEP-2002.
 XX
 XX 24-SEP-2001; 2001US-00960352.
 XX
 XX 12-JAN-1999; 99US-0115707P.
 XX 11-JAN-2000; 2000US-00480902.
 XX
 XX (BYAT//) BYATT J C.
 XX (MATH//) MATHIALAGAN N.
 XX (TAON//) TAO N.
 XX (WARR//) WARREN W C.
 XX

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XX PI Byatt JC, Mathialagan N, Tao N, Warren WC;
XX DR WPI; 2003-110599/10.
XX PT New nucleic acid associated with lactation, and muscle and fat
XX PT deposition, useful for genome mapping, gene identification and analysis,
XX PT cattle breeding, or for genetically improving cattle.
XX PS Claim 2; SEQ ID NO 7247; 245pp; English.
XX CC The invention relates to a purified nucleic acid molecule associated with
XX CC lactation or muscle and fat deposition (designated LMFD), derived from
XX CC cattle, and the LMFD nucleic acid can specifically hybridise to a second
XX CC nucleic acid molecule comprising any of 15112 nucleotide sequences,
XX CC appearing as ABX34836-ABX49947, or complements of them. Also included are
XX CC ; (1) a transformed cell having a nucleic acid comprising an LMFD nucleic
XX CC acid linked to a promoter and a 3' non- translated sequence that
XX CC functions in the cell to cause termination of transcription and addition
XX CC of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and
XX CC tissue, where hybridisation between the marker nucleic acid and the
XX CC complementary nucleic acid permits the detection of the molecule; and
XX CC (2) determining a level or pattern of a molecule in a bovine cell or
XX CC tissue comprising: (a) incubating a marker nucleic acid (comprising any
XX CC of the 15112 nucleic acid sequences or its complement or fragment) with a
XX CC complementary nucleic acid molecule obtained from the bovine cell or
XX CC tissue, where hybridisation between the marker nucleic acid and the
XX CC complementary nucleic acid permits the detection of the molecule; and
XX CC (b) determining a level or pattern of a molecule in a bovine cell or tissue.
XX CC It is useful for genome mapping, gene identification and analysis, cattle
XX CC breeding, preparation of constructs for use in cattle gene expression, or
XX CC for genetically improving cattle. The present sequence is one of the
XX CC 15112 bovine LMFD EST (expressed sequence tag) nucleic acids. Note: The
XX CC present sequence was not shown in the specification but was obtained in
XX CC electronic format from the USPTO web site:
XX CC seqdata.uspto.gov/sequence.html?DocID=20020137139
XX SQ Sequence 380 BP; 112 A; 96 C; 61 G; 111 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 8; Length 380;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TACCATGAGGACAAATATCATCTG 25
Db 174 TACCATGAGGACAAATATCATCTG 198

RESULT 6
ABX36231
ID ABX36231 standard; cDNA; 388 BP.
AC ABX36231;
AC AC
XX DT 20-FEB-2003 (first entry)
XX DE Bovine EST associated with lactation/muscle/fat deposition #1396.
XX KW Bovine; ss; EST; expressed sequence tag; lactation; LMFD;
XX KW muscle deposition; fat deposition; genome mapping; gene identification;
XX KW gene analysis; cattle breeding.
XX OS Bos Taurus.
XX PN US2002137139-A1.
XX PD 26-SEP-2002.
XX PF 24-SEP-2001; 2001US-00960352.
XX PR 12-JAN-1999; 99US-0115707P.
XX PR 11-JAN-2000; 2000US-00480902.
XX PR

XX PA (BYAT/) BYATT J C.
XX PA (MATH/) MATHIALAGAN N.
XX PA (TAON/) TAO N.
XX PA (WARR/) WARREN W C.
XX PI Byatt JC, Mathialagan N, Tao N, Warren WC;
XX XX WPI; 2003-110599/10.
XX PT New nucleic acid associated with lactation, and muscle and fat
XX PT deposition, useful for genome mapping, gene identification and analysis,
XX PT cattle breeding, or for genetically improving cattle.
XX PS Claim 2; SEQ ID NO 1396; 245pp; English.
XX CC The invention relates to a purified nucleic acid molecule associated with
XX CC lactation or muscle and fat deposition (designated LMFD), derived from
XX CC cattle, and the LMFD nucleic acid can specifically hybridise to a second
XX CC nucleic acid molecule comprising any of 15112 nucleotide sequences,
XX CC appearing as ABX34836-ABX49947, or complements of them. Also included are
XX CC ; (1) a transformed cell having a nucleic acid comprising an LMFD nucleic
XX CC acid linked to a promoter and a 3' non- translated sequence that
XX CC functions in the cell to cause termination of transcription and addition
XX CC of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and
XX CC (2) determining a level or pattern of a molecule in a bovine cell or
XX CC tissue comprising: (a) incubating a marker nucleic acid (comprising any
XX CC of the 15112 nucleic acid sequences or its complement or fragment) with a
XX CC complementary nucleic acid molecule obtained from the bovine cell or
XX CC tissue, where hybridisation between the marker nucleic acid and the
XX CC complementary nucleic acid permits the detection of the molecule; and
XX CC (b) determining a level or pattern of a molecule in a bovine cell or tissue.
XX CC It is useful for genome mapping, gene identification and analysis, cattle
XX CC breeding, preparation of constructs for use in cattle gene expression, or
XX CC for genetically improving cattle. The present sequence is one of the
XX CC 15112 bovine LMFD EST (expressed sequence tag) nucleic acids. Note: The
XX CC present sequence was not shown in the specification but was obtained in
XX CC electronic format from the USPTO web site:
XX CC seqdata.uspto.gov/sequence.html?DocID=20020137139
XX SQ Sequence 388 BP; 118 A; 111 C; 56 G; 101 T; 0 U; 2 Other;

Query Match 100.0%; Score 25; DB 8; Length 388;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TACCATGAGGACAAATATCATCTG 25
Db 109 TACCATGAGGACAAATATCATCTG 133

RESULT 7
ABX42640
ID ABX42640 standard; cDNA; 397 BP.
AC ABX42640;
AC AC
XX DT 20-FEB-2003 (first entry)
XX DE Bovine EST associated with lactation/muscle/fat deposition #7805.
XX KW Bovine; ss; EST; expressed sequence tag; lactation; LMFD;
XX KW muscle deposition; fat deposition; genome mapping; gene identification;
XX KW gene analysis; cattle breeding.
XX OS Bos Taurus.
XX PN US2002137139-A1.
XX PD 26-SEP-2002.
XX PR

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XX PF 24-SEP-2001; 2001US-00960352.
XX PR 12-JAN-1999; 99US-0115707P.
XX PR 11-JAN-2000; 2000US-00480902.
XX PA (BYAT/) BYATT J C.
XX PA (MATH/) MATHIALAGAN N.
XX PA (TAON/) TAO N.
XX PA (WARRE/) WARREN W C.
XX PI Byatt JC, Mathialagan N, Tao N, Warren WC;
XX XX WPI; 2003-110599/10.
XX XX
XX XX New nucleic acid associated with lactation, and muscle and fat
XX PT deposition, useful for genome mapping, gene identification and analysis,
XX PT cattle breeding, or for genetically improving cattle.
XX PS Claim 2; SEQ ID NO 7805; 245pp; English.
XX XX
XX CC The invention relates to a purified nucleic acid molecule associated with
XX CC lactation or muscle and fat deposition (designated LMFD), derived from
XX CC cattle, and the LMFD nucleic acid can specifically hybridise to a second
XX CC nucleic acid molecule comprising any of 1512 nucleotide sequences,
XX CC appearing as ABX34836-ABX49947, or complements of them. Also included are
XX CC ; (1) a transformed cell having a nucleic acid comprising an LMFD nucleic
XX CC acid linked to a promoter and a 3' non- translated sequence that
XX CC functions in the cell to cause termination of transcription and addition
XX CC of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and
XX CC complementary nucleic acid molecule obtained from the bovine cell or
XX CC tissue, where hybridisation between the marker nucleic acid and the
XX CC complementary nucleic acid permits the detection of the molecule; and (b)
XX CC detecting the level or pattern of the complementary nucleic acid, where
XX CC the detection of the complementary nucleic acid is predictive of the
XX CC level or pattern of the molecule. The LMFD nucleic acid is used for
XX CC determining a level or pattern of a molecule in a bovine cell or tissue.
XX CC It is useful for genome mapping, gene identification and analysis, cattle
XX CC breeding, preparation of constructs for use in cattle gene expression, or
XX CC for genetically improving cattle. The present sequence is one of the
XX CC 1512 bovine LMFD EST (expressed sequence tag) nucleic acids. Note: The
XX CC present sequence was not shown in the specification but was obtained in
XX CC electronic format from the USPTO web site:
XX CC seqdata.uspto.gov/sequence.html?DocID=20020137139
XX XX
XX SQ Sequence 397 BP; 122 A; 109 C; 58 G; 108 T; 0 U; 0 Other;
XX XX
Query Match 100.0%; Score 25; DB 8; Length 397;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TACCATGAGGACAAATATCATCTG 25
Dy 125 TACCATGAGGACAAATATCATCTG 149

RESULT 8
ABX47053
ID ABX47053 standard; cDNA; 402 BP.
XX AC ABX47053;
XX XX
XX DT 21-FEB-2003 (first entry)
XX XX
XX DB Bovine EST associated with lactation/muscle/fat deposition #12218.
XX XX
XX KW Bovine; ss; EST; expressed sequence tag; lactation; LMFD;
XX KW muscle deposition; fat deposition; genome mapping; gene identification;
XX KW gene analysis; cattle breeding.

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OS Bos Taurus.
XX US2002137139-A1.
XX PD 26-SEP-2002.
XX PF 24-SEP-2001; 2001US-00960352.
XX PR 12-JAN-1999; 99US-0115707P.
XX PR 11-JAN-2000; 2000US-00480902.
XX XX
XX PA (BYAT/) BYATT J C.
XX PA (MATH/) MATHIALAGAN N.
XX PA (TAON/) TAO N.
XX PA (WARRE/) WARREN W C.
XX XX
XX PI Byatt JC, Mathialagan N, Tao N, Warren WC;
XX XX WPI; 2003-110599/10.
XX XX
XX XX New nucleic acid associated with lactation, and muscle and fat
XX PT deposition, useful for genome mapping, gene identification and analysis,
XX PT cattle breeding, or for genetically improving cattle.
XX PS Claim 2; SEQ ID NO 12218; 245pp; English.
XX XX
XX CC The invention relates to a purified nucleic acid molecule associated with
XX CC lactation or muscle and fat deposition (designated LMFD), derived from
XX CC cattle, and the LMFD nucleic acid can specifically hybridise to a second
XX CC nucleic acid molecule comprising any of 1512 nucleotide sequences,
XX CC appearing as ABX34836-ABX49947, or complements of them. Also included are
XX CC ; (1) a transformed cell having a nucleic acid comprising an LMFD nucleic
XX CC acid linked to a promoter and a 3' non- translated sequence that
XX CC functions in the cell to cause termination of transcription and addition
XX CC of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and
XX CC complementary nucleic acid molecule obtained from the bovine cell or
XX CC tissue, where hybridisation between the marker nucleic acid and the
XX CC complementary nucleic acid permits the detection of the molecule; and (b)
XX CC detecting the level or pattern of the complementary nucleic acid, where
XX CC the detection of the complementary nucleic acid is predictive of the
XX CC level or pattern of the molecule. The LMFD nucleic acid is used for
XX CC determining a level or pattern of a molecule in a bovine cell or tissue.
XX CC It is useful for genome mapping, gene identification and analysis, cattle
XX CC breeding, preparation of constructs for use in cattle gene expression, or
XX CC for genetically improving cattle. The present sequence is one of the
XX CC 1512 bovine LMFD EST (expressed sequence tag) nucleic acids. Note: The
XX CC present sequence was not shown in the specification but was obtained in
XX CC electronic format from the USPTO web site:
XX CC seqdata.uspto.gov/sequence.html?DocID=20020137139
XX XX
XX SQ Sequence 402 BP; 125 A; 107 C; 62 G; 108 T; 0 U; 0 Other;
XX XX
Query Match 100.0%; Score 25; DB 8; Length 402;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TACCATGAGGACAAATATCATCTG 25
Dy 309 TACCATGAGGACAAATATCATCTG 333

RESULT 9
ABX44209
ID ABX44209 standard; cDNA; 409 BP.
XX AC ABX44209;
XX XX
XX DT 21-FEB-2003 (first entry)
XX XX
XX DE Bovine EST associated with lactation/muscle/fat deposition #9374.

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XX Bovine; ss; EST; expressed sequence tag; lactation; LMFD;
KW muscle deposition; fat deposition; genome mapping; gene identification;
KW gene analysis; cattle breeding.
XX Bos Taurus.
OS
XX US2002137139-A1.
XX 26-SEP-2002.
XX
XX 24-SEP-2001; 2001US-00960352.
XX
XX 12-JAN-1999; 99US-0115707P.
PR 11-JAN-2000; 2000US-00480902.
XX
XX (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
XX
PI Byatt JC, Mathialagan N, Tao N, Warren WC;
XX WPI; 2003-110599/10.
XX
XX New nucleic acid associated with lactation, and muscle and fat
PT deposition, useful for genome mapping, gene identification and analysis,
PT cattle breeding, or for genetically improving cattle.
XX
PS Claim 2; SEQ ID NO 9374; 245pp; English.
XX
XX The invention relates to a purified nucleic acid molecule associated with
CC lactation or muscle and fat deposition (designated LMFD), derived from
CC cattle, and the LMFD nucleic acid can specifically hybridise to a second
CC nucleic acid molecule comprising any of 15112 nucleotide sequences,
CC appearing as ABX34836-ABX49947, or complements of them. Also included are
CC ; (1) a transformed cell having a nucleic acid comprising an LMFD nucleic
CC acid linked to a promoter and a 3' non- translated sequence that
CC of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and
CC (2) determining a level or pattern of a molecule in a bovine cell or
CC tissue comprising: (a) incubating a marker nucleic acid (comprising any
CC of the 15112 nucleic acid sequences or its complement or fragment) with a
CC complementary nucleic acid molecule obtained from the bovine cell or
CC tissue, where hybridisation between the marker nucleic acid and the
CC complementary nucleic acid permits the detection of the molecule; and (b)
CC detecting the level or pattern of the complementary nucleic acid, where
CC the detection of the complementary nucleic acid is predictive of the
CC level or pattern of the molecule. The LMFD nucleic acid is used for
CC determining a level or pattern of a molecule in a bovine cell or tissue.
CC It is useful for genome mapping, gene identification and analysis, cattle
CC breeding, preparation of constructs for use in cattle gene expression, or
CC for genetically improving cattle. The present sequence is one of the
CC 15112 bovine LMFD EST (expressed sequence tag) nucleic acids. Note: The
CC present sequence was not shown in the specification but was obtained in
CC electronic format from the USPTO web site:
CC seqdata.uspto.gov/sequence.html?docID=20020137139
XX
SQ Sequence 409 BP; 127 A; 108 C; 62 G; 112 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 8; Length 409;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TACCATGAGGACAAATATCATCTG 25
Dn 379 TACCATGAGGACAAATATCATCTG 403

RESULT 10
ABX42249
ID ABX42249 standard; cDNA; 409 BP.
XX

AC ABX42249;
XX
XX 20-FEB-2003 (first entry)
XX
DE Bovine EST associated with lactation/muscle/fat deposition #7414.
XX
XX Bovine; ss; EST; expressed sequence tag; lactation; LMFD;
KW muscle deposition; fat deposition; genome mapping; gene identification;
KW gene analysis; cattle breeding.
XX
XX Bos Taurus.
OS
XX US2002137139-A1.
XX 26-SEP-2002.
XX
XX 24-SEP-2001; 2001US-00960352.
XX
XX 12-JAN-1999; 99US-0115707P.
PR 11-JAN-2000; 2000US-00480902.
XX
XX (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
XX
PI Byatt JC, Mathialagan N, Tao N, Warren WC;
XX WPI; 2003-110599/10.
XX
XX New nucleic acid associated with lactation, and muscle and fat
PT deposition, useful for genome mapping, gene identification and analysis,
PT cattle breeding, or for genetically improving cattle.
XX
PS Claim 2; SEQ ID NO 7414; 245pp; English.
XX
XX The invention relates to a purified nucleic acid molecule associated with
CC lactation or muscle and fat deposition (designated LMFD), derived from
CC cattle, and the LMFD nucleic acid can specifically hybridise to a second
CC nucleic acid molecule comprising any of 15112 nucleotide sequences,
CC appearing as ABX34836-ABX49947, or complements of them. Also included are
CC ; (1) a transformed cell having a nucleic acid comprising an LMFD nucleic
CC acid linked to a promoter and a 3' non- translated sequence that
CC functions in the cell to cause termination of transcription and addition
CC of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and
CC (2) determining a level or pattern of a molecule in a bovine cell or
CC tissue comprising: (a) incubating a marker nucleic acid (comprising any
CC of the 15112 nucleic acid sequences or its complement or fragment) with a
CC complementary nucleic acid molecule obtained from the bovine cell or
CC tissue, where hybridisation between the marker nucleic acid and the
CC complementary nucleic acid permits the detection of the molecule; and (b)
CC detecting the level or pattern of the complementary nucleic acid, where
CC the detection of the complementary nucleic acid is predictive of the
CC level or pattern of the molecule. The LMFD nucleic acid is used for
CC determining a level or pattern of a molecule in a bovine cell or tissue.
CC It is useful for genome mapping, gene identification and analysis, cattle
CC breeding, preparation of constructs for use in cattle gene expression, or
CC for genetically improving cattle. The present sequence is one of the
CC 15112 bovine LMFD EST (expressed sequence tag) nucleic acids. Note: The
CC present sequence was not shown in the specification but was obtained in
CC electronic format from the USPTO web site:
CC seqdata.uspto.gov/sequence.html?docID=20020137139
XX
SQ Sequence 409 BP; 128 A; 106 C; 63 G; 111 T; 0 U; 1 Other;

Query Match 100.0%; Score 25; DB 8; Length 409;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TACCATGAGGACAAATATCATCTG 25
Dn 373 TACCATGAGGACAAATATCATCTG 397

RESULT 11
ABX39507
ID ABX39507 standard; cDNA; 409 BP.
XX
AC ABX39507;
XX
AC
XX
DT 20-FEB-2003 (first entry)
XX
DE Bovine EST associated with lactation/muscle/fat deposition #4672.
XX
KW Bovine; ss; EST; expressed sequence tag; lactation; LMFD;
KW muscle deposition; fat deposition; genome mapping; gene identification;
KW gene analysis; cattle breeding.
XX
OS Bos Taurus.
XX
PN US2002137139-A1.
XX
PD 26-SEP-2002.
XX
PF 24-SEP-2001; 2001US-00960352.
XX
PR 12-JAN-1999; 99US-0115707P.
PR 11-JAN-2000; 2000US-00480902.
XX
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
XX
PI Byatt JC, Mathialagan N, Tao N, Warren WC;
XX
DR WPI; 2003-110599/10.
XX
PT New nucleic acid associated with lactation, and muscle and fat
PT deposition, useful for genome mapping, gene identification and analysis,
PT cattle breeding, or for genetically improving cattle.
XX
PS Claim 2; SEQ ID NO 4672; 245pp; English.
XX
CC The invention relates to a purified nucleic acid molecule associated with
CC lactation or muscle and fat deposition (designated LMFD), derived from
CC cattle, and the LMFD nucleic acid can specifically hybridise to a second
CC nucleic acid molecule comprising any of 15112 nucleotide sequences,
CC appearing as ABX34836-ABX49947, or complements of them. Also included are
CC ; (1) a transformed cell having a nucleic acid comprising an LMFD nucleic
CC acid linked to a promoter and a 3' non- translated sequence that
CC functions in the cell to cause termination of transcription and addition
CC of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and
CC (2) determining a level or pattern of a molecule in a bovine cell or
CC tissue, where hybridisation between the marker nucleic acid and the
CC complementary nucleic acid permits the detection of the molecule; and (b)
CC detecting the level or pattern of the complementary nucleic acid, where
CC the detection of the complementary nucleic acid is predictive of the
CC level or pattern of the molecule. The LMFD nucleic acid is used for
CC complementary nucleic acid sequences or its complement or fragment) with a
CC determining a level or pattern of a molecule in a bovine cell or tissue.
CC It is useful for genome mapping, gene identification and analysis, cattle
CC breeding, preparation of constructs for use in cattle gene expression, or
CC for genetically improving cattle. The present sequence is one of the
CC 15112 bovine LMFD EST (expressed sequence tag) nucleic acids. Note: The
CC present sequence was not shown in the USPTO web site:
CC seqdata.uspto.gov/sequence.html?DocID=20020137139
XX
SQ Sequence 409 BP; 125 A; 112 C; 61 G; 111 T; 0 U; 0 Other;
Query Match 100.0%; Score 25; DB 8; Length 409;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TACCATGAGGAGCAATATCATCTG 25
|||||
Db 340 TACCATGAGGAGCAATATCATCTG 364
XX
RESULT 12
ABX43333
ID ABX43333 standard; cDNA; 411 BP.
XX
AC ABX43333;
XX
DT 20-FEB-2003 (first entry)
XX
DE Bovine EST associated with lactation/muscle/fat deposition #8498.
XX
KW Bovine; ss; EST; expressed sequence tag; lactation; LMFD;
KW muscle deposition; fat deposition; genome mapping; gene identification;
KW gene analysis; cattle breeding.
XX
OS Bos Taurus.
XX
PN US2002137139-A1.
XX
PD 26-SEP-2002.
XX
PF 24-SEP-2001; 2001US-00960352.
XX
PR 12-JAN-1999; 99US-0115707P.
PR 11-JAN-2000; 2000US-00480902.
XX
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
XX
PI Byatt JC, Mathialagan N, Tao N, Warren WC;
XX
DR WPI; 2003-110599/10.
XX
PT New nucleic acid associated with lactation, and muscle and fat
PT deposition, useful for genome mapping, gene identification and analysis,
PT cattle breeding, or for genetically improving cattle.
XX
PS Claim 2; SEQ ID NO 8498; 245pp; English.
XX
CC The invention relates to a purified nucleic acid molecule associated with
CC lactation or muscle and fat deposition (designated LMFD), derived from
CC cattle, and the LMFD nucleic acid can specifically hybridise to a second
CC nucleic acid molecule comprising any of 15112 nucleotide sequences,
CC appearing as ABX34836-ABX49947, or complements of them. Also included are
CC ; (1) a transformed cell having a nucleic acid comprising an LMFD nucleic
CC acid linked to a promoter and a 3' non- translated sequence that
CC functions in the cell to cause termination of transcription and addition
CC of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and
CC (2) determining a level or pattern of a molecule in a bovine cell or
CC tissue comprising: (a) incubating a marker nucleic acid (comprising any
CC of the 15112 nucleic acid sequences or its complement or fragment) with a
CC complementary nucleic acid molecule obtained from the bovine cell or
CC tissue, where hybridisation between the marker nucleic acid and the
CC complementary nucleic acid permits the detection of the molecule; and (b)
CC detecting the level or pattern of the complementary nucleic acid, where
CC the detection of the complementary nucleic acid is predictive of the
CC level or pattern of the molecule. The LMFD nucleic acid is used for
CC determining a level or pattern of a molecule in a bovine cell or tissue.
CC It is useful for genome mapping, gene identification and analysis, cattle
CC breeding, preparation of constructs for use in cattle gene expression, or
CC for genetically improving cattle. The present sequence is one of the
CC 15112 bovine LMFD EST (expressed sequence tag) nucleic acids. Note: The
CC present sequence was not shown in the USPTO web site:
CC seqdata.uspto.gov/sequence.html?DocID=20020137139
XX

SQ Sequence 411 BP; 130 A; 109 C; 61 G; 111 T; 0 U; 0 Other;
 Query Match 100.0%; Score 25; DB 8; Length 411;
 Best Local Similarity 100.0%; Pred. No. 0.27; 0; Indels 0; Gaps 0;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TACCATGAGGACAAATATCATCTCTG 25
 |||||
 DB 378 TACCATGAGGACAAATATCATCTCTG 402
 |||||

RESULT 13
 ABX35955
 ID ABX35955 standard; cDNA; 412 BP.
 XX AC ABX35955;
 XX 20-FEB-2003 (first entry)
 XX Bovine EST associated with lactation/muscle/fat deposition #1120.
 XX KW Bovine; ss; EST; expressed sequence tag; lactation; LMFD;
 KW muscle deposition; fat deposition; genome mapping; gene identification;
 KW gene analysis; cattle breeding.
 XX OS Bos Taurus.
 XX US2002137139-A1.
 XX 26-SEP-2002.
 XX 24-SEP-2001; 2001US-00960352.
 XX 12-JAN-1999; 99US-0115707P.
 XX 11-JAN-2000; 2000US-00480902.
 XX (BYAT/) BYATT J C.
 PA (MATH/) MATHIALAGAN N.
 PA (TAON/) TAO N.
 PA (WARR/) WARREN W C.
 XX Byatt JC, Mathialagan N, Tao N, Warren WC;
 WPI; 2003-110599/10.
 XX New nucleic acid associated with lactation, and muscle and fat
 PT deposition, useful for genome mapping, gene identification and analysis,
 PT cattle breeding, or for genetically improving cattle.
 XX Claim 2; SEQ ID NO 1120; 245pp; English.
 XX The invention relates to a purified nucleic acid molecule associated with
 CC lactation or muscle and fat deposition (designated LMFD), derived from
 CC cattle, and the LMFD nucleic acid can specifically hybridise to a second
 CC nucleic acid molecule comprising any of 15112 nucleotide sequences,
 CC appearing as ABX34836-ABX49947, or complements of them. Also included are
 CC ; (1) a transformed cell having a nucleic acid comprising an LMFD nucleic
 CC acid linked to a promoter and a 3' non- translated sequence that
 CC functions in the cell to cause termination of transcription and addition
 CC of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and
 CC (2) determining a level or pattern of a molecule in a bovine cell or
 CC tissue comprising: (a) incubating a marker nucleic acid (comprising any
 CC of the 15112 nucleic acid sequences or its complement or fragment) with a
 CC complementary nucleic acid molecule obtained from the bovine cell or
 CC tissue, where hybridisation between the marker nucleic acid and the
 CC complementary nucleic acid permits the detection of the molecule; and
 CC detecting the level or pattern of the complementary nucleic acid, where
 CC It is useful for genome mapping, gene identification and analysis, cattle
 CC breeding, preparation of constructs for use in cattle gene expression, or
 CC for genetically improving cattle. The present sequence is one of the

CC 15112 bovine LMFD EST (expressed sequence tag) nucleic acids. Note: The
 CC present sequence was not shown in the specification but was obtained in
 CC electronic format from the USPTO web site:
 CC seqdata.uspto.gov/sequence.html?DocID=20020137139
 XX SQ Sequence 412 BP; 118 A; 108 C; 61 G; 125 T; 0 U; 0 Other;
 Query Match 100.0%; Score 25; DB 8; Length 412;
 Best Local Similarity 100.0%; Pred. No. 0.27; 0; Indels 0; Gaps 0;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TACCATGAGGACAAATATCATCTCTG 25
 |||||
 DB 372 TACCATGAGGACAAATATCATCTCTG 396
 |||||

RESULT 14
 ABX37092
 ID ABX37092 standard; cDNA; 413 BP.
 XX AC ABX37092;
 XX 20-FEB-2003 (first entry)
 XX Bovine EST associated with lactation/muscle/fat deposition #2257.
 XX KW Bovine; ss; EST; expressed sequence tag; lactation; LMFD;
 KW muscle deposition; fat deposition; genome mapping; gene identification;
 KW gene analysis; cattle breeding.
 XX OS Bos Taurus.
 XX US2002137139-A1.
 XX 26-SEP-2002.
 XX 24-SEP-2001; 2001US-00960352.
 XX 12-JAN-1999; 99US-0115707P.
 XX 11-JAN-2000; 2000US-00480902.
 XX (BYAT/) BYATT J C.
 PA (MATH/) MATHIALAGAN N.
 PA (TAON/) TAO N.
 PA (WARR/) WARREN W C.
 XX Byatt JC, Mathialagan N, Tao N, Warren WC;
 WPI; 2003-110599/10.
 XX New nucleic acid associated with lactation, and muscle and fat
 PT deposition, useful for genome mapping, gene identification and analysis,
 PT cattle breeding, or for genetically improving cattle.
 XX Claim 2; SEQ ID NO 2257; 245pp; English.
 XX The invention relates to a purified nucleic acid molecule associated with
 CC lactation or muscle and fat deposition (designated LMFD), derived from
 CC cattle, and the LMFD nucleic acid can specifically hybridise to a second
 CC nucleic acid molecule comprising any of 15112 nucleotide sequences,
 CC appearing as ABX34836-ABX49947, or complements of them. Also included are
 CC ; (1) a transformed cell having a nucleic acid comprising an LMFD nucleic
 CC acid linked to a promoter and a 3' non- translated sequence that
 CC functions in the cell to cause termination of transcription and addition
 CC of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and
 CC (2) determining a level or pattern of a molecule in a bovine cell or
 CC tissue comprising: (a) incubating a marker nucleic acid (comprising any
 CC of the 15112 nucleic acid sequences or its complement or fragment) with a
 CC complementary nucleic acid molecule obtained from the bovine cell or
 CC tissue, where hybridisation between the marker nucleic acid and the
 CC complementary nucleic acid permits the detection of the molecule; and (b)
 CC detecting the level or pattern of the complementary nucleic acid, where
 CC the detection of the complementary nucleic acid is predictive of the

CC level or pattern of the molecule. The LMFD nucleic acid is used for
 CC determining a level or pattern of a molecule in a bovine cell or tissue.
 CC It is useful for genome mapping, gene identification and analysis, cattle
 CC breeding, preparation of constructs for use in cattle gene expression, or
 CC for genetically improving cattle. The present sequence is one of the
 CC 15112 bovine LMFD EST (expressed sequence tag) nucleic acids. Note: The
 CC present sequence was not shown in the specification but was obtained in
 CC electronic format from the USPTO web site:
 CC seqdata.uspto.gov/sequence.html?DocID=20020137139
 XX
 SQ Sequence 413 BP; 130 A; 109 C; 62 G; 112 T; 0 U; 0 Other;
 Query Match 100.0%; Score 25; DB 8; Length 413;
 Best Local Similarity 100.0%; Pred. No. 0.27;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TACCATGAGGACAAATATCATCTCTG 25
 Db 384 TACCATGAGGACAAATATCATCTCTG 408
 RESULT 15
 ABX46099
 ID ABX46099 standard; cDNA; 414 BP.
 XX
 AC ABX46099;
 XX
 DT 21-FEB-2003 (first entry)
 XX
 DE Bovine EST associated with lactation/muscle/fat deposition #11264.
 XX
 KW Bovine; ss; EST; expressed sequence tag; lactation; LMFD;
 KW muscle deposition; fat deposition; genome mapping; gene identification;
 KW gene analysis; cattle breeding.
 XX
 OS Bos Taurus.
 XX
 PN US2002137139-A1.
 XX
 PD 26-SEP-2002.
 XX
 PF 24-SEP-2001; 2001US-00960352.
 XX
 PR 12-JAN-1999; 99US-0115707P.
 PR 11-JAN-2000; 2000US-00480902.
 XX
 PA (BYAT/) BYATT J C.
 PA (MATH/) MATHIALAGAN N.
 PA (TAON/) TAO N.
 PA (WARR/) WARREN W C.
 XX
 PI Byatt JC, Mathialagan N, Tao N, Warren WC;
 XX
 DR WPI; 2003-110599/10.
 XX
 PT New nucleic acid associated with lactation, and muscle and fat
 PT deposition, useful for genome mapping, gene identification and analysis,
 PT cattle breeding, or for genetically improving cattle.
 XX
 PS Claim 2; SEQ ID NO 11264; 245pp; English.
 XX
 CC The invention relates to a purified nucleic acid molecule associated with
 CC lactation or muscle and fat deposition (designated LMFD), derived from
 CC cattle, and the LMFD nucleic acid can specifically hybridise to a second
 CC nucleic acid molecule comprising any of 15112 nucleotide sequences,
 CC appearing as ABX34836-ABX49947, or complements of them. Also included are
 CC : (1) a transformed cell having a nucleic acid comprising an LMFD nucleic
 CC acid linked to a promoter and a 3' non- translated sequence that
 CC functions in the cell to cause termination of transcription and addition
 CC of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and
 CC (2) determining a level or pattern of a molecule in a bovine cell or
 CC tissue comprising: (a) incubating a marker nucleic acid (comprising any
 CC of the 15112 nucleic acid sequences or its complement or fragment) with a

CC complementary nucleic acid molecule obtained from the bovine cell or
 CC tissue, where hybridisation between the marker nucleic acid and the
 CC complementary nucleic acid permits the detection of the molecule; and (b)
 CC detecting the level or pattern of the complementary nucleic acid, where
 CC the detection of the complementary nucleic acid is predictive of the
 CC level or pattern of the molecule. The LMFD nucleic acid is used for
 CC determining a level or pattern of a molecule in a bovine cell or tissue.
 CC It is useful for genome mapping, gene identification and analysis, cattle
 CC breeding, preparation of constructs for use in cattle gene expression, or
 CC for genetically improving cattle. The present sequence is one of the
 CC 15112 bovine LMFD EST (expressed sequence tag) nucleic acids. Note: The
 CC present sequence was not shown in the specification but was obtained in
 CC electronic format from the USPTO web site:
 CC seqdata.uspto.gov/sequence.html?DocID=20020137139
 XX
 SQ Sequence 414 BP; 130 A; 110 C; 61 G; 113 T; 0 U; 0 Other;
 Query Match 100.0%; Score 25; DB 8; Length 414;
 Best Local Similarity 100.0%; Pred. No. 0.27;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TACCATGAGGACAAATATCATCTCTG 25
 Db 384 TACCATGAGGACAAATATCATCTCTG 408
 Search completed: November 17, 2004, 00:09:08
 Job time : 43.7744 secs

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OM nucleic - nucleic search, using sw model

Run on: November 16, 2004, 23:55:00 ; Search time 8.89101 Seconds
(without alignments)
1998.616 Million cell updates/sec

Title: US-09-821-782E-1

Perfect score: 25

Sequence: 1 taccatgagacaaatattcattctg 25

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents NA:*

1: /cgn2_6/ptodata/1/ina/5A COMB.seq.*

2: /cgn2_6/ptodata/1/ina/5B COMB.seq.*

3: /cgn2_6/ptodata/1/ina/6A COMB.seq.*

4: /cgn2_6/ptodata/1/ina/6B COMB.seq.*

5: /cgn2_6/ptodata/1/ina/PTCUS COMB.seq.*

6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21.8	87.2	759	4	US-09-270-767-11513
2	20.2	80.8	255	4	US-09-702-705-719
3	20.2	80.8	255	4	US-09-736-457-719
4	20.2	80.8	255	4	US-09-614-124B-719
5	20.2	80.8	255	4	US-09-671-325-719
6	20.2	80.8	255	4	US-09-589-184-719
7	20.2	80.8	255	4	US-09-658-824-719
8	20.2	80.8	1140	4	US-09-377-497-7
9	20.2	80.8	16568	4	US-09-525-906-1
10	20.2	80.8	16569	3	US-09-097-889-2
11	20.2	80.8	16569	3	US-09-377-856-1
12	20.2	80.8	16569	4	US-09-302-681-2
13	20.2	80.8	16569	4	US-09-098-079-2
14	20.2	80.8	16569	4	US-10-053-611-1
15	20	80.0	34	1	US-07-825-959-8
16	20	80.0	34	1	US-08-131-324-8
17	20	80.0	34	1	US-08-647-584-6
18	20	80.0	34	3	US-09-358-972-255
19	20	80.0	34	3	US-09-406-064-48
20	20	80.0	34	3	US-09-383-316-95
21	20	80.0	34	4	US-09-788-847-48
22	20	80.0	34	4	US-09-790-417-255
23	18.4	73.6	20	1	US-08-647-584-9
24	18.4	73.6	20	1	US-08-647-584-11
25	18.2	72.8	3176	2	US-08-910-733-17
26	18.2	72.8	3176	2	US-08-910-884-17
27	17.8	71.2	1624	1	US-08-255-670A-1

28	17.6	70.4	26	1	US-07-971-160-35	Sequence 35, Appl
29	17.6	70.4	26	1	US-08-336-241-35	Sequence 35, Appl
30	17.6	70.4	26	2	US-08-465-273-35	Sequence 35, Appl
31	17.6	70.4	26	2	US-09-119-024-35	Sequence 35, Appl
32	17.6	70.4	26	2	US-08-417-226-35	Sequence 35, Appl
33	17.6	70.4	26	3	US-09-196-131-35	Sequence 35, Appl
34	17.6	70.4	26	3	US-08-643-732-35	Sequence 35, Appl
35	17.6	70.4	26	4	US-09-836-169-35	Sequence 35, Appl
36	17	68.0	286	4	US-09-313-294A-4131	Sequence 4131, Ap
37	17	68.0	292	4	US-09-313-294A-4131	Sequence 4131, Ap
38	17	68.0	1637	4	US-09-270-767-27053	Sequence 27053, A
39	17	68.0	3264	4	US-09-270-767-11466	Sequence 11466, A
40	17	68.0	16950	3	US-09-453-702B-166	Sequence 166, App
41	17	68.0	1230025	4	US-09-198-452A-1	Sequence 1, Appl
42	16.8	67.2	1067	4	US-09-369-247-29	Sequence 29, Appl
43	16.6	66.4	224	2	US-08-569-166-26	Sequence 26, Appl
44	16.6	66.4	717	4	US-09-489-039A-2273	Sequence 2273, Ap
45	16.6	66.4	1434	4	US-09-700-397-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1

US-09-270-767-11513
; Sequence 11513, Application US/09270767

; Patent No. 6703491

; GENERAL INFORMATION:

; APPLICANT: Homburger et al.

; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster

; FILE REFERENCE: File Reference: 7326-094

; CURRENT APPLICATION NUMBER: US/09/270,767

; CURRENT FILING DATE: 1999-03-17

; NUMBER OF SEQ ID NOS: 62517

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 11513

; LENGTH: 759

; TYPE: DNA

; ORGANISM: Drosophila melanogaster

US-09-270-767-11513

Query Match 87.2%; Score 21.8; DB 4; Length 759;

Best Local Similarity 92.0%; Pred. No. 0.52;

Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TACCATGAGACAAATATCATTCG 25

Db 656 TACCTTGAGGACAAATATCATTTG 680

RESULT 2

US-09-702-705-719

; Sequence 719, Application US/09702705

; Patent No. 6504010

; GENERAL INFORMATION:

; APPLICANT: Wang, Tongtong

; APPLICANT: Bangur, Chaitanya S.

; APPLICANT: Lodes, Michael A.

; APPLICANT: Fanger, Gary

; APPLICANT: Vedvick, Tom

; APPLICANT: Carter, Darrick

; APPLICANT: Retter, Marc

; APPLICANT: Mannion, Jane

; APPLICANT: Fan, Liqun

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

; FILE REFERENCE: 210121.478C14

; CURRENT APPLICATION NUMBER: US/09/702,705

; CURRENT FILING DATE: 2000-10-30

; NUMBER OF SEQ ID NOS: 1833

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 719

; LENGTH: 255

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; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(255)
; OTHER INFORMATION: n = A,T,C or G
US-09-702-705-719

Query Match      80.8%; Score 20.2; DB 4; Length 255;
Best Local Similarity 88.0%; Pred. No. 2.4;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TACCATGAGGACAAATATCATCTG 25
   |||||
Db 96 TCCCGTGAGGCCAAATATCATCTG 120

RESULT 3
US-09-736-457-719
; Sequence 719, Application US/09736457
; Patent No. 6509448
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedwick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; APPLICANT: Wang, Aijun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.478C15
; CURRENT APPLICATION NUMBER: US/09/736,457
; CURRENT FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 1864
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 719
; LENGTH: 255
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(255)
; OTHER INFORMATION: n = A,T,C or G
US-09-736-457-719

Query Match      80.8%; Score 20.2; DB 4; Length 255;
Best Local Similarity 88.0%; Pred. No. 2.4;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TACCATGAGGACAAATATCATCTG 25
   |||||
Db 96 TCCCGTGAGGCCAAATATCATCTG 120

RESULT 4
US-09-614-124B-719
; Sequence 719, Application US/09614124B
; Patent No. 6630574
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedwick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.478C15
; CURRENT APPLICATION NUMBER: US/09/614,124B
; CURRENT FILING DATE: 2000-09-26
; NUMBER OF SEQ ID NOS: 1825
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 719
; LENGTH: 255
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(255)
; OTHER INFORMATION: n = A,T,C or G
US-09-614-124B-719

Query Match      80.8%; Score 20.2; DB 4; Length 255;
Best Local Similarity 88.0%; Pred. No. 2.4;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TACCATGAGGACAAATATCATCTG 25
   |||||
Db 96 TCCCGTGAGGCCAAATATCATCTG 120

RESULT 5
US-09-671-325-719
; Sequence 719, Application US/09671325
; Patent No. 6667154
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedwick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.478C12
; CURRENT APPLICATION NUMBER: US/09/671,325
; CURRENT FILING DATE: 2000-09-26
; NUMBER OF SEQ ID NOS: 1825
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 719
; LENGTH: 255
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(255)
; OTHER INFORMATION: n = A,T,C or G
US-09-671-325-719

Query Match      80.8%; Score 20.2; DB 4; Length 255;
Best Local Similarity 88.0%; Pred. No. 2.4;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TACCATGAGGACAAATATCATCTG 25
   |||||
Db 96 TCCCGTGAGGCCAAATATCATCTG 120

RESULT 6
US-09-589-184-719
; Sequence 719, Application US/09589184
; Patent No. 6686447
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
```

; FACILE NO. 621611/
 ; GENERAL INFORMATION:
 ; APPLICANT: Herrstadt, Corrina
 ; APPLICANT: Ghosh, Soumitra S.

APPLICANT: Davis, Robert E.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING
TITLE OF INVENTION: AGENTS THAT QUANTITATIVELY ALTER DETECTABLE
TITLE OF INVENTION: EXTRAMITOCHONDRIAL DNA: MITOCHONDRIAL DNA RATIOS
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSER: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/097,889
FILING DATE: 15-JUN-1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Roseman Ph.D., Stephen J.
REGISTRATION NUMBER: 43,058
REFERENCE/DOCKET NUMBER: 660088.417
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 16569 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-097-889-2

Query Match 80.8%; Score 20.2; DB 3; Length 16569;
Best Local Similarity 88.0%; Pred. No. 5.2;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TACCATGAGGACAAATATCAATCTG 25
Db 15144 TCCCGTGAGGCCAAATATCAATCTG 15168

RESULT 11
US-09-377-856-1
Sequence 1, Application US/09377856
Patent No. 6344322
GENERAL INFORMATION:
APPLICANT: Polyak, Kornelia
APPLICANT: Vogelstein, Bert
APPLICANT: Kinzler, Kenneth
TITLE OF INVENTION: Subtle Mitochondrial Mutations as Tumor
FILE REFERENCE: 1107.82346
CURRENT APPLICATION NUMBER: US/09/377,856
PRIOR FILING DATE: 1999-08-20
PRIOR APPLICATION NUMBER: 60/097,307
PRIOR FILING DATE: 1998-08-20
NUMBER OF SEQ ID NOS: 1
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1
LENGTH: 16569
TYPE: DNA
ORGANISM: Homo sapiens
US-09-377-856-1
Query Match 80.8%; Score 20.2; DB 3; Length 16569;
Best Local Similarity 88.0%; Pred. No. 5.2;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 TACCATGAGGACAAATATCAATCTG 25

Db 15144 TCCCGTGAGGCCAAATATCAATCTG 15168
RESULT 12
US-09-302-681-2
Sequence 2, Application US/09302681
Patent No. 6441149
GENERAL INFORMATION:
APPLICANT: HerinStadt, Corrina
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Clevenger, William
APPLICANT: Fahy, Eoin F.
APPLICANT: Davis, Robert E.
TITLE OF INVENTION: DIAGNOSTIC METHOD BASED ON
TITLE OF INVENTION: QUANTIFICATION OF EXTRAMITOCHONDRIAL DNA
FILE REFERENCE: 660088.416C1
CURRENT APPLICATION NUMBER: US/09/302,681
CURRENT FILING DATE: 1999-04-30
NUMBER OF SEQ ID NOS: 108
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 16569
TYPE: DNA
ORGANISM: Homo sapien
US-09-302-681-2

Query Match 80.8%; Score 20.2; DB 4; Length 16569;
Best Local Similarity 88.0%; Pred. No. 5.2;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 TACCATGAGGACAAATATCAATCTG 25
Db 15144 TCCCGTGAGGCCAAATATCAATCTG 15168

RESULT 13
US-09-098-079-2
Sequence 2, Application US/09098079
Patent No. 6489095
GENERAL INFORMATION:
APPLICANT: HerinStadt, Corrina
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Clevenger, William
APPLICANT: Fahy, Eoin F.
APPLICANT: Davis, Robert E.
TITLE OF INVENTION: DIAGNOSTIC METHOD BASED ON QUANTIFICATION OF
TITLE OF INVENTION: EXTRAMITOCHONDRIAL DNA
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/098,079
FILING DATE: 15-JUN-1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Roseman Ph.D., Stephen J.
REGISTRATION NUMBER: 43,058
REFERENCE/DOCKET NUMBER: 660088.416
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 2:


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;
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 16569 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
US-09-098-079-2

Query Match      80.8%; Score 20.2; DB 4; Length 16569;
Best Local Similarity 88.0%; Pred. No. 5.2;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TACCATGAGGACAAATATCATTTCTG 25
Db 15144 TCCCGTGAGGCCAAATATCATTTCTG 15168

RESULT 14
US-10-053-611-1
; Sequence 1, Application US/10053611
; Patent No. 6756021
; GENERAL INFORMATION:
; APPLICANT: Polyak, Kornelia
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; TITLE OF INVENTION: Subtle Mitochondrial Mutations as Tumor
; TITLE OF INVENTION: Markers
; FILE REFERENCE: 1107.82346
; CURRENT APPLICATION NUMBER: US/10/053.611
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: US/09/377,856
; PRIOR FILING DATE: 1999-08-20
; PRIOR APPLICATION NUMBER: 60/097,307
; PRIOR FILING DATE: 1998-08-20
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 16569
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-053-611-1

Query Match      80.8%; Score 20.2; DB 4; Length 16569;
Best Local Similarity 88.0%; Pred. No. 5.2;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TACCATGAGGACAAATATCATTTCTG 25
Db 15144 TCCCGTGAGGCCAAATATCATTTCTG 15168

RESULT 15
US-07-825-959-8/c
; Sequence 8, Application US/07825959
; Patent No. 5372929
; GENERAL INFORMATION:
; APPLICANT: Cimino, George C.
; APPLICANT: Lin, Lily
; TITLE OF INVENTION: METHOD FOR MEASURING THE INACTIVATION OF
; TITLE OF INVENTION: PATHOGENS
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Limbach & Limbach
; STREET: 2001 Ferry Building
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
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;
; APPLICATION NUMBER: US/07/825,959
; FILING DATE: 19920127
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
;   NAME: Weseman, James C
;   REGISTRATION NUMBER: 30,507
;   REFERENCE/DOCKET NUMBER: HRI-02200
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 433-4150
; TELEFAX: (415) 433-8716
; TELEX: 278356
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 34 base pairs
;   TYPE: NUCLEIC ACID
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: DNA (genomic)
;   FRAGMENT TYPE: internal
US-07-825-959-8

Query Match      80.0%; Score 20; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 TGAGGACAAATATCATTTCTG 25
Db 34 TGAGGACAAATATCATTTCTG 15

Search completed: November 17, 2004, 03:15:09
Job time : 12.891 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 16, 2004, 16:25:24 ; Search time 42.4054 Seconds
(without alignments)
3218.578 Million cell updates/sec

Title: US-09-821-782E-2

Perfect score: 26

Sequence: 1 cctcctagtgttagggattgatcg 26

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N_Geneseq_23Sep04:*
1: Geneseqn1980s:*
2: Geneseqn1990s:*
3: Geneseqn2000s:*
4: Geneseqn2001as:*
5: Geneseqn2001bs:*
6: Geneseqn2002as:*
7: Geneseqn2002bs:*
8: Geneseqn2003as:*
9: Geneseqn2003bs:*
10: Geneseqn2003cs:*
11: Geneseqn2003ds:*
12: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	26	100.0	26	8	Abq83298 Cytochrom
2	26	100.0	472	8	Abq83306 Mitochond
3	26	100.0	472	8	Abq83307 Mitochond
4	24.4	93.8	200	8	Abx44247 Bovine ES
5	24.4	93.8	235	8	Abx38797 Bovine ES
6	24.4	93.8	241	8	Abx40252 Bovine ES
7	24.4	93.8	331	8	Abx38833 Bovine ES
8	24.4	93.8	411	8	Abx46901 Bovine ES
9	24.4	93.8	416	8	Abx44048 Bovine ES
10	24.4	93.8	417	8	Abx47842 Bovine ES
11	24.4	93.8	419	8	Abx37167 Bovine ES
12	24.4	93.8	448	8	Abx43592 Bovine ES
13	24.4	93.8	469	8	Abx35993 Bovine ES
14	24.4	93.8	472	8	Abq83314 Mitochond
15	24.4	93.8	472	8	Abq83313 Mitochond
16	24.4	93.8	472	8	Abq83327 Mitochond
17	24.4	93.8	472	8	Abq83296 Antelope
18	24.4	93.8	472	8	Abq83317 Mitochond
19	24.4	93.8	472	8	Abq83321 Mitochond
20	24.4	93.8	472	8	Abq83332 Mitochond
21	24.4	93.8	472	8	Abq83329 Mitochond

Abq83328 Mitochond
Abq83303 Mitochond
Abq83304 Mitochond
Abq83326 Mitochond
Abq83337 Mitochond
Abx40046 Bovine ES
Abn74229 Bovine em
Aaa43716 Human sec
Acd93024 Human col
Abi37235 Human col
Acd92164 Human col
Abv08925 Human pro
Abv12642 Human pro
Acd92416 Human col
Aai82841 Human pol
Aai8354 Human pol
Aai8787 Human pol
Acd93031 Human col
Aai88933 Human pol
Aai8049 Human adu
Aai87673 Human pol
Abv95467 Human pan
Aai81714 Human pol
Abv95916 Human pan

ALIGNMENTS

RESULT 1
ABQ83298
ID ABQ83298 standard; DNA; 26 BP.
XX
AC ABQ83298;
XX
DT 18-JAN-2003 (first entry)
XX
DE Cytochrome b gene universal PCR primer mcb 369 SEQ ID NO:3.
XX
KW Mitochondrial cytochrome b gene; mitochondrial; cytochrome b;
KW identification; criminal investigation; animal poaching; PCR primer; ss.
XX
OS Synthetic.
XX
PN W0200277278-A1.
XX
PD 03-OCT-2002.
XX
PF 28-MAR-2001; 2001WO-IN000055.
XX
PR 28-MAR-2001; 2001WO-IN000055.
XX
(COUL) COUNCIL SCI & IND RES.
XX
PA Verma SK, Singh L;
XX
PI WPI; 2003-018945/01.
XX
PT New universal primers, mcb 398 and mcb 869, capable of amplifying a
PT fragment of cytochrome b gene of any animal species, useful for
PT establishing the identity of biological materials and animals for
PT molecular evidence in forensics.
XX
PS Claim 1; Page 116; 128pp; English.
XX
CC The present invention describes universal primers, mcb 398 and mcb 869
CC (see ABQ83297 and ABQ83298), capable of amplifying a fragment of
CC cytochrome b gene of any animal species in polymerase chain reaction
CC (PCR) and revealing the identity of the biological material of any animal
CC of unknown origin at species and sub-species level. Also described is a
CC method for the identification of the animal from a biological sample. The
CC method is used for animal identification to establish the crime with the
CC criminal beyond a reasonable doubt, to establish the identity of

CC biological materials such as skin, horns confiscated from animal
 CC poachers, if it is that of an endangered species, for the purpose of
 CC molecular evidence of animal hunting and related crime in the court of
 CC law, so that human violation of the wildlife resources could be
 CC controlled, to have an idea of the geographical location of the
 CC commitment of wildlife crime based on the cytochrome b gene haplotype of
 CC poached animal identified by the universal primer invented, to detect the
 CC adulteration of animal meat in food products for the purpose of food
 CC fortification, by the food fortification agencies, to provide a universal
 CC technique for detection of the origin of blood or blood stains collected
 CC from the scene of the crime related to offenses such as murder and rape,
 CC in order to establish the origin of blood found at the scene of the crime
 CC when it sounds as if criminals intentionally spread the blood of an
 CC animal at the scene of the crime to confuse the crime investigators and
 CC forensic scientists with human blood, and so that the method can be
 CC converted to a commercial molecular kit and DNA chips based applications
 CC for wildlife identification in forensics
 XX
 SQ Sequence 26 BP; 4 A; 5 C; 7 G; 10 T; 0 U; 0 Other;

Query Match 100.0%; Score 26; DB 8; Length 26;
 Best Local Similarity 100.0%; Pred. No. 0.025;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTCCTAGTTTGTAGGGATTGATCG 26
 |||||
 DB 1 CCTCCTAGTTTGTAGGGATTGATCG 26

RESULT 2
 ABQ83306/c
 ID ABQ83306 standard; DNA; 472 BP.
 XX
 AC ABQ83306;
 XX
 DT 18-JAN-2003 (first entry)
 XX
 DE Mitochondrial cytochrome b gene sequence SEQ ID NO:11.
 XX
 KW Mitochondrial cytochrome b gene; mitochondrial; cytochrome b;
 KW identification; criminal investigation; animal poaching; gene; ds.
 XX
 OS Unidentified.
 XX
 PN WO200277278-A1.
 XX
 PD 03-OCT-2002.
 XX
 PF 28-MAR-2001; 2001WO-IN000055.
 XX
 PR 28-MAR-2001; 2001WO-IN000055.
 XX
 PA (COUL) COUNCIL SCI & IND RES.
 XX
 PI Verma SK, Singh L;
 XX
 DR WPI; 2003-018945/01.
 XX

PT New universal primers, mcb 398 and mcb 869, capable of amplifying a
 PT fragment of cytochrome b gene of any animal species, useful for
 PT establishing the identity of biological materials and animals for
 PT molecular evidence in forensics.
 XX

PS Example 1; Page 28-57; 128pp; English.

XX The present invention describes universal primers, mcb 398 and mcb 869
 CC (see ABQ83297 and ABQ83298), capable of amplifying a fragment of
 CC cytochrome b gene of any animal species in polymerase chain reaction
 CC (PCR) and revealing the identity of the biological material of any animal
 CC of unknown origin at species and sub-species level. Also described is a
 CC method for the identification of the animal from a biological sample. The
 CC method is used for animal identification to establish the crime with the
 CC criminal beyond a reasonable doubt, to establish the identity of

CC biological materials such as skin, horns confiscated from animal
 CC poachers, if it is that of an endangered species, for the purpose of
 CC molecular evidence of animal hunting and related crime in the court of
 CC law, so that human violation of the wildlife resources could be
 CC controlled, to have an idea of the geographical location of the
 CC commitment of wildlife crime based on the cytochrome b gene haplotype of
 CC poached animal identified by the universal primer invented, to detect the
 CC adulteration of animal meat in food products for the purpose of food
 CC fortification, by the food fortification agencies, to provide a universal
 CC technique for detection of the origin of blood or blood stains collected
 CC from the scene of the crime related to offenses such as murder and rape,
 CC in order to establish the origin of blood found at the scene of the crime
 CC when it sounds as if criminals intentionally spread the blood of an
 CC animal at the scene of the crime to confuse the crime investigators and
 CC forensic scientists with human blood, and so that the method can be
 CC converted to a commercial molecular kit and DNA chips based applications
 CC for wildlife identification in forensics. The present sequence represents
 CC a mitochondrial cytochrome b gene sequence from the present invention
 XX
 SQ Sequence 472 BP; 140 A; 153 C; 66 G; 113 T; 0 U; 0 Other;

Query Match 100.0%; Score 26; DB 8; Length 472;
 Best Local Similarity 100.0%; Pred. No. 0.034;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTCCTAGTTTGTAGGGATTGATCG 26
 |||||
 DB 472 CCTCCTAGTTTGTAGGGATTGATCG 447

RESULT 3
 ABQ83307/c
 ID ABQ83307 standard; DNA; 472 BP.
 XX
 AC ABQ83307;
 XX
 DT 18-JAN-2003 (first entry)
 XX
 DE Mitochondrial cytochrome b gene sequence SEQ ID NO:12.
 XX
 KW Mitochondrial cytochrome b gene; mitochondrial; cytochrome b;
 KW identification; criminal investigation; animal poaching; gene; ds.
 XX
 OS Unidentified.
 XX
 PN WO200277278-A1.
 XX
 PD 03-OCT-2002.
 XX
 PF 28-MAR-2001; 2001WO-IN000055.
 XX
 PR 28-MAR-2001; 2001WO-IN000055.
 XX
 PA (COUL) COUNCIL SCI & IND RES.
 XX
 PI Verma SK, Singh L;
 XX
 DR WPI; 2003-018945/01.
 XX

PT New universal primers, mcb 398 and mcb 869, capable of amplifying a
 PT fragment of cytochrome b gene of any animal species, useful for
 PT establishing the identity of biological materials and animals for
 PT molecular evidence in forensics.
 XX

PS Example 1; Page 28-57; 128pp; English.

XX The present invention describes universal primers, mcb 398 and mcb 869
 CC (see ABQ83297 and ABQ83298), capable of amplifying a fragment of
 CC cytochrome b gene of any animal species in polymerase chain reaction
 CC (PCR) and revealing the identity of the biological material of any animal
 CC of unknown origin at species and sub-species level. Also described is a
 CC method for the identification of the animal from a biological sample. The
 CC method is used for animal identification to establish the crime with the
 CC method is used for animal identification to establish the crime with the

CC criminal beyond a reasonable doubt, to establish the identity of
 CC biological materials such as skin, horns confiscated from animal
 CC poachers, if it is that of an endangered species, for the purpose of
 CC molecular evidence of animal hunting and related crime in the court of
 CC law, so that human violation of the wildlife resources could be
 CC controlled, to have an idea of the geographical location of the
 CC commitment of wildlife crime based on the cytochrome b gene haplotype of
 CC poached animal identified by the universal primer invented, to detect the
 CC adulteration of animal meat in food products for the purpose of food
 CC fortification, by the food fortification agencies, to provide a universal
 CC technique for detection of the origin of blood or blood stains collected
 CC from the scene of the crime related to offenses such as murder and rape,
 CC in order to establish the origin of blood found at the scene of the crime
 CC when it sounds as if criminals intentionally spread the blood of an
 CC animal at the scene of the crime to confuse the crime investigators and
 CC forensic scientists with human blood, and so that the method can be
 CC converted to a commercial molecular kit and DNA chips based applications
 CC for wildlife identification in forensics. The present sequence represents
 CC a mitochondrial cytochrome b gene sequence from the present invention
 XX
 XX Sequence 472 BP; 141 A; 153 C; 66 G; 112 T; 0 U; 0 Other;

Query Match 100.0%; Score 26; DB 8; Length 472;
 Best Local Similarity 100.0%; Pred. No. 0.034;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTCCTAGTTTGTAGGATTGATCG 26
 DB 472 CCTCCTAGTTTGTAGGATTGATCG 447

RESULT 4
 ABX44247/c
 ID ABX44247 standard; cDNA; 200 BP.
 XX
 AC ABX44247;
 XX
 DT 21-FEB-2003 (first entry)
 DE Bovine EST associated with lactation/muscle/fat deposition #9412.
 XX
 KW Bovine; ss; EST; expressed sequence tag; lactation; LMFD;
 KW muscle deposition; fat deposition; genome mapping; gene identification;
 KW gene analysis; cattle breeding.
 XX
 OS Bos Taurus.

XX US2002137139-A1.
 XX 26-SEP-2002.
 XX 24-SEP-2001; 2001US-00960352.
 XX 12-JAN-1999; 99US-0115707P.
 XX 11-JAN-2000; 2000US-00480902.
 XX
 PA (BYAT/) BYATT J C.
 PA (MATH/) MATHIALAGAN N.
 PA (TAON/) TAO N.
 PA (WARR/) WARREN W C.
 XX
 PI Byatt JC, Mathialagan N, Tao N, Warren WC;
 XX WPI; 2003-110599/10.
 XX
 XX New nucleic acid associated with lactation, and muscle and fat
 PT deposition, useful for genome mapping, gene identification and analysis,
 PT cattle breeding, or for genetically improving cattle.
 XX
 PS Claim 2; SEQ ID NO 9412; 245pp; English.
 XX
 CC The invention relates to a purified nucleic acid molecule associated with
 CC lactation or muscle and fat deposition (designated LMFD), derived from

CC cattle, and the LMFD nucleic acid can specifically hybridise to a second
 CC nucleic acid molecule comprising any of 15112 nucleotide sequences,
 CC appearing as ABX34836-ABX49947, or complements of them. Also included are
 CC ; (1) a transformed cell having a nucleic acid comprising an LMFD nucleic
 CC acid linked to a promoter and a 3' non- translated sequence that
 CC functions in the cell to cause termination of transcription and addition
 CC of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and
 CC (2) determining a level or pattern of a molecule in a bovine cell or
 CC tissue comprising: (a) incubating a marker nucleic acid (comprising any
 CC of the 15112 nucleic acid sequences or its complement or fragment) with a
 CC complementary nucleic acid molecule obtained from the bovine cell or
 CC tissue, where hybridisation between the marker nucleic acid and the
 CC complementary nucleic acid permits the detection of the molecule; and (b)
 CC detecting the level or pattern of the complementary nucleic acid, where
 CC the detection of the complementary nucleic acid is predictive of the
 CC level or pattern of the molecule. The LMFD nucleic acid is used for
 CC determining a level or pattern of a molecule in a bovine cell or tissue.
 CC It is useful for genome mapping, gene identification and analysis, cattle
 CC breeding, preparation of constructs for use in cattle gene expression, or
 CC for genetically improving cattle. The present sequence is one of the
 CC 15112 bovine LMFD EST (expressed sequence tag) nucleic acids. Note: The
 CC present sequence was not shown in the specification but was obtained in
 CC electronic format from the USPTO web site:
 CC seqdata.uspto.gov/sequence.html?DocID=200201371139
 XX
 XX Sequence 200 BP; 62 A; 66 C; 28 G; 44 T; 0 U; 0 Other;

Query Match 93.8%; Score 24.4; DB 8; Length 200;
 Best Local Similarity 96.2%; Pred. No. 0.17;
 Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCTCCTAGTTTGTAGGATTGATCG 26
 DB 36 CCTCCTAGTTTGTAGGATTGATCG 11

RESULT 5
 ABX38797/c
 ID ABX38797 standard; cDNA; 235 BP.
 XX
 AC ABX38797;
 XX
 DT 20-FEB-2003 (first entry)
 XX
 DE Bovine EST associated with lactation/muscle/fat deposition #3962.
 XX
 KW Bovine; ss; EST; expressed sequence tag; lactation; LMFD;
 KW muscle deposition; fat deposition; genome mapping; gene identification;
 KW gene analysis; cattle breeding.
 XX
 OS Bos Taurus.
 XX
 PN US2002137139-A1.
 XX 26-SEP-2002.
 XX 24-SEP-2001; 2001US-00960352.
 XX 12-JAN-1999; 99US-0115707P.
 XX 11-JAN-2000; 2000US-00480902.
 XX
 PA (BYAT/) BYATT J C.
 PA (MATH/) MATHIALAGAN N.
 PA (TAON/) TAO N.
 PA (WARR/) WARREN W C.
 XX
 PI Byatt JC, Mathialagan N, Tao N, Warren WC;
 XX WPI; 2003-110599/10.
 XX
 XX New nucleic acid associated with lactation, and muscle and fat
 PT deposition, useful for genome mapping, gene identification and analysis,
 PT cattle breeding, or for genetically improving cattle.

XX PS Claim 2; SEQ ID NO 3962; 245pp; English.

XX CC The invention relates to a purified nucleic acid molecule associated with lactation or muscle and fat deposition (designated LMFD), derived from cattle, and the LMFD nucleic acid can specifically hybridise to a second nucleic acid molecule comprising any of 15112 nucleotide sequences, appearing as ABX34836-ABX49947, or complements of them. Also included are (1) a transformed cell having a nucleic acid comprising an LMFD nucleic acid linked to a promoter and a 3' non-translated sequence that functions in the cell to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and (2) determining a level or pattern of a molecule in a bovine cell or tissue comprising: (a) incubating a marker nucleic acid (comprising any of the 15112 nucleic acid sequences or its complement or fragment) with a complementary nucleic acid molecule obtained from the bovine cell or tissue, where hybridisation between the marker nucleic acid and the complementary nucleic acid permits the detection of the molecule; and (b) detecting the level or pattern of the complementary nucleic acid, where the detection of the complementary nucleic acid is predictive of the level or pattern of the molecule. The LMFD nucleic acid is used for determining a level or pattern of a molecule in a bovine cell or tissue. It is useful for genome mapping, gene identification and analysis, cattle breeding, preparation of constructs for use in cattle gene expression, or for genetically improving cattle. The present sequence is one of the 15112 bovine LMFD EST (expressed sequence tag) nucleic acids. Note: The present sequence was not shown in the specification but was obtained in electronic format from the USPTO web site: seqdata.uspto.gov/sequence.html?DocID=20020137139

XX CC Sequence 235 BP; 76 A; 76 C; 27 G; 56 T; 0 U; 0 Other;

XX CC Query Match 93.8%; Score 24.4; DB 8; Length 235;

XX CC Best Local Similarity 96.2%; Pred. No. 0.18; Length 235;

XX CC Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCTCTAGTTTGTAGGGATTGATCG 26

DB 144 CCTCTAGTTTGTAGGGATTGATCG 119

RESULT 6

ABX40252/c

ID ABX40252 standard; cDNA; 241 BP.

XX AC ABX40252;

XX DT 20-FEB-2003 (first entry)

XX DE Bovine EST associated with lactation/muscle/fat deposition #5417.

XX KW Bovine; ss; EST; expressed sequence tag; lactation; LMFD;

XX KW muscle deposition; fat deposition; genome mapping; gene identification;

XX KW gene analysis; cattle breeding.

XX OS Bos Taurus.

XX PN US2002137139-A1.

XX PD 26-SEP-2002.

XX PF 24-SEP-2001; 2001US-00960352.

XX PR 12-JAN-1999; 99US-0115707P.

XX PR 11-JAN-2000; 2000US-00480902.

XX PA (BYATT/) BYATT J C.

XX PA (MATH/) MATHIALAGAN N.

XX PA (TAON/) TAO N.

XX PA (WARR/) WARREN W C.

XX PI Byatt JC, Mathialagan N, Tao N, Warren WC;

XX PA (MATH/) MATHIALAGAN N.

DR WPI; 2003-110599/10.

XX CC New nucleic acid associated with lactation, and muscle and fat deposition, useful for genome mapping, gene identification and analysis, cattle breeding, or for genetically improving cattle.

XX PS Claim 2; SEQ ID NO 5417; 245pp; English.

XX CC The invention relates to a purified nucleic acid molecule associated with lactation or muscle and fat deposition (designated LMFD), derived from cattle, and the LMFD nucleic acid can specifically hybridise to a second nucleic acid molecule comprising any of 15112 nucleotide sequences, appearing as ABX34836-ABX49947, or complements of them. Also included are (1) a transformed cell having a nucleic acid comprising an LMFD nucleic acid linked to a promoter and a 3' non-translated sequence that functions in the cell to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and (2) determining a level or pattern of a molecule in a bovine cell or tissue comprising: (a) incubating a marker nucleic acid (comprising any of the 15112 nucleic acid sequences or its complement or fragment) with a complementary nucleic acid molecule obtained from the bovine cell or tissue, where hybridisation between the marker nucleic acid and the complementary nucleic acid permits the detection of the molecule; and (b) detecting the level or pattern of the complementary nucleic acid, where the detection of the complementary nucleic acid is predictive of the level or pattern of the molecule. The LMFD nucleic acid is used for determining a level or pattern of a molecule in a bovine cell or tissue. It is useful for genome mapping, gene identification and analysis, cattle breeding, preparation of constructs for use in cattle gene expression, or for genetically improving cattle. The present sequence is one of the 15112 bovine LMFD EST (expressed sequence tag) nucleic acids. Note: The present sequence was not shown in the specification but was obtained in electronic format from the USPTO web site: seqdata.uspto.gov/sequence.html?DocID=20020137139

XX CC Sequence 241 BP; 75 A; 82 C; 27 G; 57 T; 0 U; 0 Other;

XX CC Query Match 93.8%; Score 24.4; DB 8; Length 241;

XX CC Best Local Similarity 96.2%; Pred. No. 0.18; Length 241;

XX CC Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCTCTAGTTTGTAGGGATTGATCG 26

DB 96 CCTCTAGTTTGTAGGGATTGATCG 71

RESULT 7

ABX38833/c

ID ABX38833 standard; cDNA; 331 BP.

XX AC ABX38833;

XX DT 20-FEB-2003 (first entry)

XX DE Bovine EST associated with lactation/muscle/fat deposition #3998.

XX KW Bovine; ss; EST; expressed sequence tag; lactation; LMFD;

XX KW muscle deposition; fat deposition; genome mapping; gene identification;

XX KW gene analysis; cattle breeding.

XX OS Bos Taurus.

XX PN US2002137139-A1.

XX PD 26-SEP-2002.

XX PF 24-SEP-2001; 2001US-00960352.

XX PR 12-JAN-1999; 99US-0115707P.

XX PR 11-JAN-2000; 2000US-00480902.

XX PA (BYATT/) BYATT J C.

XX PA (MATH/) MATHIALAGAN N.

XX PD 26-SEP-2002.
 XX OS
 XX PF 24-SEP-2001; 2001US-00960352.
 XX PN 12-JAN-1999; 99US-0115707P.
 XX PR 11-JAN-2000; 2000US-00480902.
 XX PD 26-SEP-2002.
 XX PF 24-SEP-2001; 2001US-00960352.
 XX PR 12-JAN-1999; 99US-0115707P.
 XX PR 11-JAN-2000; 2000US-00480902.
 XX PA (BYATT/) BYATT J C.
 XX PA (MATH/) MATHIALAGAN N.
 XX PA (TAON/) TAO N.
 XX PA (WARR/) WARREN W C.
 XX PI Byatt JC, Mathialagan N, Tao N, Warren WC;
 XX WPI; 2003-110599/10.
 XX DR
 XX PT New nucleic acid associated with lactation, and muscle and fat
 PT deposition, useful for genome mapping, gene identification and analysis,
 PT cattle breeding, or for genetically improving cattle.
 XX PS Claim 2; SEQ ID NO 9213; 245pp; English.
 XX CC The invention relates to a purified nucleic acid molecule associated with
 CC lactation or muscle and fat deposition (designated LMFD), derived from
 CC cattle, and the LMFD nucleic acid can specifically hybridise to a second
 CC nucleic acid molecule comprising any of 15112 nucleotide sequences,
 CC appearing as ABX34836-ABX49947, or complements of them. Also included are
 CC ; (1) a transformed cell having a nucleic acid comprising an LMFD nucleic
 CC acid linked to a promoter and a 3' non- translated sequence that
 CC functions in the cell to cause termination of transcription and addition
 CC of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and
 CC (2) determining a level or pattern of a molecule in a bovine cell or
 CC tissue comprising: (a) incubating a marker nucleic acid (comprising any
 CC of the 15112 nucleic acid sequences or its complement or fragment) with a
 CC complementary nucleic acid molecule obtained from the bovine cell or
 CC tissue, where hybridisation between the marker nucleic acid and the
 CC complementary nucleic acid permits the detection of the molecule; and (b)
 CC detecting the level or pattern of the complementary nucleic acid, where
 CC the detection of the complementary nucleic acid is predictive of the
 CC level or pattern of the molecule. The LMFD nucleic acid is used for
 CC determining a level or pattern of a molecule in a bovine cell or tissue.
 CC It is useful for genome mapping, gene identification and analysis, cattle
 CC breeding, preparation of constructs for use in cattle gene expression, or
 CC for genetically improving cattle. The present sequence is one of the
 CC 15112 bovine LMFD EST (expressed sequence tag) nucleic acids. Note: The
 CC present sequence was not shown in the specification but was obtained in
 CC electronic format from the USPTO web site:
 CC seqdata.uspto.gov/sequence.html?DocID=20020137139
 XX SQ Sequence 416 BP; 138 A; 132 C; 57 G; 89 T; 0 U; 0 Other;
 Query Match 93.8%; Score 24.4; DB 8; Length 416;
 Best Local Similarity 96.2%; Pred. No. 0.19;
 Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CCTCCTAGTTGTTAGGATTGATCG 26
 |||||
 DB 115 CCTCCTAGTTGTTAGGATTGATCG 90
 RESULT 10
 ABX47842/c
 ID ABX47842 standard; cDNA; 417 BP.
 XX AC ABX47842;
 XX XX
 XX DT 21-FEB-2003 (first entry)
 XX DE Bovine EST associated with lactation/muscle/fat deposition #13007.
 XX KW Bovine; ss; EST; expressed sequence tag; lactation; LMFD;
 KW muscle deposition; fat deposition; genome mapping; gene identification;

KW gene analysis; cattle breeding.
 XX OS
 XX PF 26-SEP-2002.
 XX PN 24-SEP-2001; 2001US-00960352.
 XX PR 12-JAN-1999; 99US-0115707P.
 XX PR 11-JAN-2000; 2000US-00480902.
 XX PA (BYATT/) BYATT J C.
 XX PA (MATH/) MATHIALAGAN N.
 XX PA (TAON/) TAO N.
 XX PA (WARR/) WARREN W C.
 XX PI Byatt JC, Mathialagan N, Tao N, Warren WC;
 XX WPI; 2003-110599/10.
 XX DR
 XX PT New nucleic acid associated with lactation, and muscle and fat
 PT deposition, useful for genome mapping, gene identification and analysis,
 PT cattle breeding, or for genetically improving cattle.
 XX PS Claim 2; SEQ ID NO 13007; 245pp; English.
 XX CC The invention relates to a purified nucleic acid molecule associated with
 CC lactation or muscle and fat deposition (designated LMFD), derived from
 CC cattle, and the LMFD nucleic acid can specifically hybridise to a second
 CC nucleic acid molecule comprising any of 15112 nucleotide sequences,
 CC appearing as ABX34836-ABX49947, or complements of them. Also included are
 CC ; (1) a transformed cell having a nucleic acid comprising an LMFD nucleic
 CC acid linked to a promoter and a 3' non- translated sequence that
 CC functions in the cell to cause termination of transcription and addition
 CC of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and
 CC (2) determining a level or pattern of a molecule in a bovine cell or
 CC tissue comprising: (a) incubating a marker nucleic acid (comprising any
 CC of the 15112 nucleic acid sequences or its complement or fragment) with a
 CC complementary nucleic acid molecule obtained from the bovine cell or
 CC tissue, where hybridisation between the marker nucleic acid and the
 CC complementary nucleic acid permits the detection of the molecule; and (b)
 CC detecting the level or pattern of the complementary nucleic acid, where
 CC the detection of the complementary nucleic acid is predictive of the
 CC level or pattern of the molecule. The LMFD nucleic acid is used for
 CC determining a level or pattern of a molecule in a bovine cell or tissue.
 CC It is useful for genome mapping, gene identification and analysis, cattle
 CC breeding, preparation of constructs for use in cattle gene expression, or
 CC for genetically improving cattle. The present sequence is one of the
 CC 15112 bovine LMFD EST (expressed sequence tag) nucleic acids. Note: The
 CC present sequence was not shown in the specification but was obtained in
 CC electronic format from the USPTO web site:
 CC seqdata.uspto.gov/sequence.html?DocID=20020137139
 XX SQ Sequence 417 BP; 137 A; 138 C; 53 G; 89 T; 0 U; 0 Other;
 Query Match 93.8%; Score 24.4; DB 8; Length 417;
 Best Local Similarity 96.2%; Pred. No. 0.19;
 Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CCTCCTAGTTGTTAGGATTGATCG 26
 |||||
 DB 152 CCTCCTAGTTGTTAGGATTGATCG 127
 RESULT 11
 ABX37167/c
 ID ABX37167 standard; cDNA; 419 BP.
 XX AC ABX37167;
 XX XX
 XX DT 20-FEB-2003 (first entry)

XX DE Bovine EST associated with lactation/muscle/fat deposition #2332.
XX AC
XX KW Bovine; ss; EST; expressed sequence tag; lactation; LMFD;
KW muscle deposition; fat deposition; genome mapping; gene identification;
KW gene analysis; cattle breeding.
XX OS
XX Bos Taurus.
XX PN US2002137139-A1.
XX PD 26-SEP-2002.
XX PF 24-SEP-2001; 2001US-00960352.
XX PR 12-JAN-1999; 99US-0115707P.
XX PR 11-JAN-2000; 2000US-00480902.
XX PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
XX Byatt JC, Mathialagan N, Tao N, Warren WC;
XX WPI; 2003-110599/10.
XX
XX New nucleic acid associated with lactation, and muscle and fat
PT deposition, useful for genome mapping, gene identification and analysis,
PT cattle breeding, or for genetically improving cattle.
XX
XX Claim 2; SEQ ID NO 2332; 245pp; English.
XX
XX The invention relates to a purified nucleic acid molecule associated with
CC lactation or muscle and fat deposition (designated LMFD), derived from
CC cattle, and the LMFD nucleic acid can specifically hybridise to a second
CC nucleic acid molecule comprising any of 15112 nucleotide sequences,
CC appearing as ABX34836-ABX49947, or complements of them. Also included are
CC ; (1) a transformed cell having a nucleic acid comprising an LMFD nucleic
CC acid linked to a promoter and a 3' non- translated sequence that
CC functions in the cell to cause termination of transcription and addition
CC of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and
CC (2) determining a level or pattern of a molecule in a bovine cell or
CC tissue comprising: (a) incubating a marker nucleic acid (comprising any
CC of the 15112 nucleic acid sequences or its complement or fragment) with a
CC complementary nucleic acid molecule obtained from the bovine cell or
CC tissue, where hybridisation between the marker nucleic acid and the
CC complementary nucleic acid molecule permits the detection of the molecule; and
CC detecting the level or pattern of the complementary nucleic acid, where
CC the detection of the complementary nucleic acid is predictive of the
CC level or pattern of the molecule. The LMFD nucleic acid is used for
CC determining a level or pattern of a molecule in a bovine cell or tissue.
CC It is useful for genome mapping, gene identification and analysis, cattle
CC breeding, preparation of constructs for use in cattle gene expression, or
CC for genetically improving cattle. The present sequence is one of the
CC 15112 bovine LMFD EST (expressed sequence tag) nucleic acids. Note: The
CC present sequence was not shown in the specification but was obtained in
CC electronic format from the USPTO web site:
CC seqdata.uspto.gov/sequence.html?DocID=20020137139
XX
XX SQ Sequence 419 BP; 123 A; 141 C; 53 G; 102 T; 0 U; 0 Other;

Query Match 93.8%; Score 24.4; DB 8; Length 419;
Best Local Similarity 96.2%; Pred. No. 0.19;
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCTCCTAGTTGTTAGGGATTGATCG 26
Db 194 CCTCCTAGTTGTTAGGGATTGATCG 169

RESULT 12
ABX43592/c

ID ABX43592 standard; cDNA; 448 BP.
XX AC
XX ABX43592;
XX DT 21-FEB-2003 (first entry)
XX KE Bovine EST associated with lactation/muscle/fat deposition #8757.
XX DE
XX KW Bovine; ss; EST; expressed sequence tag; lactation; LMFD;
KW muscle deposition; fat deposition; genome mapping; gene identification;
KW gene analysis; cattle breeding.
XX OS
XX Bos Taurus.
XX PN US2002137139-A1.
XX PD 26-SEP-2002.
XX PF 24-SEP-2001; 2001US-00960352.
XX PR 12-JAN-1999; 99US-0115707P.
XX PR 11-JAN-2000; 2000US-00480902.
XX PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
XX Byatt JC, Mathialagan N, Tao N, Warren WC;
XX WPI; 2003-110599/10.
XX
XX New nucleic acid associated with lactation, and muscle and fat
PT deposition, useful for genome mapping, gene identification and analysis,
PT cattle breeding, or for genetically improving cattle.
XX
XX Claim 2; SEQ ID NO 8757; 245pp; English.
XX
XX The invention relates to a purified nucleic acid molecule associated with
CC lactation or muscle and fat deposition (designated LMFD), derived from
CC cattle, and the LMFD nucleic acid can specifically hybridise to a second
CC nucleic acid molecule comprising any of 15112 nucleotide sequences,
CC appearing as ABX34836-ABX49947, or complements of them. Also included are
CC ; (1) a transformed cell having a nucleic acid comprising an LMFD nucleic
CC acid linked to a promoter and a 3' non- translated sequence that
CC functions in the cell to cause termination of transcription and addition
CC of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and
CC (2) determining a level or pattern of a molecule in a bovine cell or
CC tissue comprising: (a) incubating a marker nucleic acid (comprising any
CC of the 15112 nucleic acid sequences or its complement or fragment) with a
CC complementary nucleic acid molecule obtained from the bovine cell or
CC tissue, where hybridisation between the marker nucleic acid and the
CC complementary nucleic acid molecule permits the detection of the molecule; and
CC detecting the level or pattern of the complementary nucleic acid, where
CC the detection of the complementary nucleic acid is predictive of the
CC level or pattern of the molecule. The LMFD nucleic acid is used for
CC determining a level or pattern of a molecule in a bovine cell or tissue.
CC It is useful for genome mapping, gene identification and analysis, cattle
CC breeding, preparation of constructs for use in cattle gene expression, or
CC for genetically improving cattle. The present sequence is one of the
CC 15112 bovine LMFD EST (expressed sequence tag) nucleic acids. Note: The
CC present sequence was not shown in the specification but was obtained in
CC electronic format from the USPTO web site:
CC seqdata.uspto.gov/sequence.html?DocID=20020137139
XX
XX SQ Sequence 448 BP; 131 A; 146 C; 55 G; 116 T; 0 U; 0 Other;

Query Match 93.8%; Score 24.4; DB 8; Length 448;
Best Local Similarity 96.2%; Pred. No. 0.19;
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCTCCTAGTTGTTAGGGATTGATCG 26
|||||
|||||

Query Match 93.8%; Score 24.4; DB 8; Length 469;

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OM nucleic - nucleic search, using sw model

Run on: November 16, 2004, 22:24:28 ; Search time 343.642 Seconds
(without alignments)
2650.992 Million cell updates/sec

Title: US-09-821-782E-1

Perfect score: 25

Sequence: 1 taccatgagacaaatattcttg 25

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: gb_est1.*
2: gb_est2.*
3: gb_btc.*
4: gb_est3.*
5: gb_est4.*
6: gb_est5.*
7: gb_est6.*
8: gb_gss1.*
9: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25	100.0	130	6	CB219995 1Abo10D11
2	25	100.0	315	5	CB060285 4010439 B
3	25	100.0	328	7	CF615703 CES014188
4	25	100.0	338	1	AU277825 AU277825
5	25	100.0	361	4	BM430528 1Duo35F3.
6	25	100.0	398	2	BE589920 196607 BA
7	25	100.0	398	4	BG688078 335513 BA
8	25	100.0	408	4	BM433056 1JEU9D3.a
9	25	100.0	411	5	BP112175 BP112175
10	25	100.0	413	4	BM433038 1JEU9B6.a
11	25	100.0	414	6	CB225030 10M28R03
12	25	100.0	431	5	BP110134 BP110134
13	25	100.0	432	1	AV613710 AV613710
14	25	100.0	432	1	AV663157 AV663157
15	25	100.0	436	6	CB060174 4010727 B
16	25	100.0	438	2	BF430396 934 MARC
17	25	100.0	442	2	BE483891 170238 BA
18	25	100.0	442	6	CB220057 1Abo16G09
19	25	100.0	442	7	CN791814 4126609 B
20	25	100.0	445	2	BF429564 1105 MARC
21	25	100.0	446	2	BF429555 1095 MARC
22	25	100.0	448	2	BF429532 1068 MARC
23	25	100.0	448	6	CB221459 1Duo11H10
24	25	100.0	453	5	BP112710 BP112710

25	100.0	456	7	CN432453	CN432453 BE0200010
26	100.0	462	4	BM480699	BM480699 531379 MA
27	100.0	467	7	CN822416	CN822416 Oa_splbn_MA
28	100.0	468	2	BF604803	BF604803 270971 MA
29	100.0	477	4	BM430220	BM430220 1Duo31D6.
30	100.0	479	5	BP110300	BP110300 BP110300
31	100.0	482	7	CF931047	CF931047 CF--06-R-
32	100.0	483	4	BM432066	BM432066 1JEU16A10
33	100.0	484	4	BM445456	BM445456 11L11FL2.
34	100.0	484	6	CB220685	CB220685 1Abo25C08
35	100.0	484	6	CB223613	CB223613 1JEU25F2
36	100.0	485	2	BF889654	BF889654 289202 MA
37	100.0	485	6	CB224011	CB224011 1JEU30D2
38	100.0	486	6	CB221941	CB221941 11L21H5 B
39	100.0	487	4	BM434623	BM434623 1R111A03
40	100.0	489	2	BF652253	BF652253 275762 MA
41	100.0	490	6	CB221081	CB221081 1Abo30A09
42	100.0	491	6	CB223477	CB223477 1JEU23H6
43	100.0	492	4	BM429985	BM429985 1Duo28A12
44	100.0	493	6	CB222631	CB222631 11L30B01
45	100.0	496	5	BP110116	BP110116 BP110116

ALIGNMENTS

RESULT 1
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LOCUS CB219995 130 bp mRNA linear EST 10-FEB-2003
DEFINITION 1Abo10D11 Bos taurus Abomasum #1 library Bos taurus CDNA, mRNA
sequence.
ACCESSION CB219995
VERSION CB219995.1 GI:28290509
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
REFERENCE 1 (bases 1 to 130)
AUTHORS Hansen, C., Fu, A., Meng, Y., Li, C., Okine, E., Sensen, C.W.,
Gordon, P.M.K. and Moore, S.S.
TITLE Gene Expression Profiling of the Bovine Gastrointestinal Tract
JOURNAL Unpublished (2002)
COMMENT Contact: Dr. Stephen Moore
Beef Genomics Laboratory
Dept of AFNS, University of Alberta
410 Agri/For, Dept of AFNS, U of A, Edmonton, AB, T6G 2P5, Canada
Tel: 780 492 0169
Fax: 780 492 4265
Email: stephen.moore@ualberta.ca
Insert Length: 130 Std Error: 0.00
POLYA=Yes.

FEATURES

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/dev_stage="Young adult"
/lab_host="X11-BlueMRF"-strain"
/clone_lib="Bos taurus Abomasum #1 library"
/note="Organ: Abomasum; Vector: Uni-2ZAPXR; Site_1: EcoR
I; Site_2: Xho I"

ORIGIN

Query Match 100.0%; Score 25; DB 6; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.89;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TACCATGAGCAAAATATCATTCGT 25
|||||

Db 52 TACCATGAGGACAAATATCATCTG 76

RESULT 2

LOCUS CB060285/c 315 bp mRNA linear EST 17-JAN-2003
DEFINITION 4010439 BARC-EMBRAPA 326BOV Bos indicus cDNA clone 326BOV_1005
Unknown, mRNA sequence.

ACCESSION CB060285
VERSION CB060285.1 GI:27798572
KEYWORDS EST.
SOURCE Bos indicus (zebu)
ORGANISM Bos indicus

REFERENCE 1 (bases 1 to 315)
AUTHORS da Mota,A.F., Sonstegard,T.S., Van Tassel,C.P., Matukumalli,L.K., Wood,D.L., Capuco,A.V., Brito,M.A.P., Martinez,M.L., Connor,E.E., Machado,M.A. and Coutinho,L.L.

TITLE Construction and Characterization of cDNA Libraries Generated from Mammary Gland Tissues of Holstein (Bos taurus) and Gir (Bos indicus) Cattle
JOURNAL Unpublished (2002)
COMMENT Contact: Adilson F. da Mota
Gene Evaluation and Mapping Laboratory
USDA, ARS, Animal and Natural Resources Institute
Bldg. 200 Rm3 BARC-East, Beltsville, MD 20705, USA
Tel: 3015048456
Fax: 3015048414
Email: amota@ncp1.embrapa.br

Single pass sequencing. Bases called and trimmed with phred
0.00925 using options -trim alt '' -trim fasta. Vector identified
by cross_match using options -mismatch 12 -mismatch 12
PCR Primers
FORWARD: GTTTCCCGAGTCACGAGTTG
BACKWARD: TGAGCGGATACAAATTCACACAG

Seq: 1 row: 0 column: 05
Seq primer: GTTTTCCCGAGTCACGAGTTG
High quality sequence stop: 315.
Location/Qualifiers
1..315
/organism="Bos indicus"
/mol_type="mRNA"
/strain="Brazilian Dairy Gir"
/db_xref="taxon:9915"
/clone="326BOV_1005"
/sex="female"
/tissue_type="parenchyma"
/cell_type="epithelium"
/dev_stage="involved"
/lab_host="DH5alpha"
/clone_lib="BARC-EMBRAPA 326BOV"

/note="Organ: mammary; Vector: pUC 118; Site 1: HincII;
Site 2: HincII; This mammary-derived cDNA library was
created as part of a collaborative project between the ARS
Gene Evaluation and Mapping Laboratory and the EMBRAPA
Dairy Cattle Research Center under the sponsorship of
USDA, ARS/EMBRAPA-LABEX program in animal genomics. RNA
sample from cow AM1, samples 2, 4, and 5 extracted on
3/27/02, RT with Superscript II at 37 deg C annealing
temperature, PCR with 16-mers."

FEATURES

source
1..315
Location/Qualifiers
1..315
/organism="Bos indicus"
/mol_type="mRNA"
/strain="Brazilian Dairy Gir"
/db_xref="taxon:9915"
/clone="326BOV_1005"
/sex="female"
/tissue_type="parenchyma"
/cell_type="epithelium"
/dev_stage="involved"
/lab_host="DH5alpha"
/clone_lib="BARC-EMBRAPA 326BOV"

/note="Organ: mammary; Vector: pUC 118; Site 1: HincII;
Site 2: HincII; This mammary-derived cDNA library was
created as part of a collaborative project between the ARS
Gene Evaluation and Mapping Laboratory and the EMBRAPA
Dairy Cattle Research Center under the sponsorship of
USDA, ARS/EMBRAPA-LABEX program in animal genomics. RNA
sample from cow AM1, samples 2, 4, and 5 extracted on
3/27/02, RT with Superscript II at 37 deg C annealing
temperature, PCR with 16-mers."

ORIGIN

Query Match 100.0%; Score 25; DB 6; Length 315;
Best Local Similarity 100.0%; Pred. No. 0.98;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TACCATGAGGACAAATATCATCTG 25
|||||

Db 202 TACCATGAGGACAAATATCATCTG 178
|||||

RESULT 3

LOCUS CF615703 328 bp mRNA linear EST 01-OCT-2003
DEFINITION CES014188 Bos taurus muscle cDNA library Bos taurus cDNA clone
CCL013263 5', mRNA sequence.

ACCESSION CF615703
VERSION CF615703.1 GI:37242577
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus

REFERENCE 1 (bases 1 to 328)
AUTHORS Wang,Y.H., Byrne,K., Vuocolo,T., Tan,S.H., McWilliam,S., Dierens,L.
and Lehnert,S.

TITLE Transcription profiling of bovine skeletal muscle and subcutaneous fat
JOURNAL Unpublished (2003)
COMMENT Contact: Dr Sigr id Lehnert
Functional Genomics Lab
CSIRO Livestock Industries
Level 5, Queensland Bioscience Precinct, University of Queensland,
306 Carmody Road St.Lucia QLD Australia
Tel: 07 3214 2445
Fax: 07 3214 2480
Email: Sigr id.Lehnert@csiro.au
Plate: 12 row: H column: 05.

FEATURES

source
1..328
Location/Qualifiers
1..328
/organism="Bos taurus"
/mol_type="mRNA"
/strain="Angus"
/db_xref="taxon:9913"
/clone="CCL013263"
/sex="male"
/tissue_type="Longissimus dorsi muscle"
/dev_stage="Young Adult"
/lab_host="XLI-BlueMRF'strain"
/clone_lib="Bos taurus muscle cDNA library"
/note="Organ: skeletal muscle; Vector: Uni-ZAPXR; Site 1:
EcoRI; Site 2: Xho I; Library made from skeletal muscle of
a 14 month old Angus steer."

ORIGIN

Query Match 100.0%; Score 25; DB 7; Length 328;
Best Local Similarity 100.0%; Pred. No. 0.99;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TACCATGAGGACAAATATCATCTG 25
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Db 38 TACCATGAGGACAAATATCATCTG 62
|||||

RESULT 4

LOCUS AU277825/c 338 bp mRNA linear EST 02-JUL-2002
DEFINITION AU277825 Cloned bovine fetus cDNA Bos taurus cDNA clone fetus37511
3', mRNA sequence.

ACCESSION AU277825
VERSION AU277825.1 GI:21681135
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus

REFERENCE 1 (bases 1 to 338)
AUTHORS Oishi,M., Yamada,T., Goma,H., Lejukole,H.Y., Taniguchi,Y. and
Sasaki,Y.

TITLE EST analysis of cloned bovine fetus and placenta
JOURNAL Unpublished (2002)
COMMENT Contact: Masahito Oishi

Graduate School of Agriculture
Kyoto University
Sakyoku Kitashirakawa, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-6331
Fax: 81-75-753-6340
Email: oishi@kajs.jkns.kais.kyoto-u.ac.jp.

FEATURES

source

1. .338
Location/Qualifiers
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/clone="fetus37E11"
/dev_stage="fetus"
/clone_lib="Cloned bovine fetus cdna"

ORIGIN

Query Match 100.0%; Score 25; DB 1; Length 338;
Best Local Similarity 100.0%; Pred. No. 0.99;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TACCATGAGCAAAATATCATCTG 25
|||||
DB 230 TACCATGAGCAAAATATCATCTG 206

RESULT 5

LOCUS

BM430528 361 bp mRNA linear EST 31-JAN-2002
1Du035F3.abl Bos taurus Duodenum #1 library Bos taurus cdna, mRNA
sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Bos taurus (cow)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.

REFERENCE

1 (bases 1 to 361)

AUTHORS

Hansen, C., Fu, A., Meng, Y., Li, C., Okine, E., Sensen, C.W.,
Gordon, P.M.K. and Moore, S.S.

TITLE

Gene Expression Profiling of the Bovine Gastrointestinal Tract

JOURNAL

COMMENT

Unpublished (2002)
Contact: Dr. Stephen Moore
Beef Genomics Laboratory
Dept of AFNS, University of Alberta
410 Agri/For, Dept of AFNS, U of A, Edmonton, AB, T6G 2P5, Canada
Tel: 780 492 0169
Fax: 780 492 4265

Email: stephen.moore@ualberta.ca

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FEATURES

source

1. .361
Location/Qualifiers
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/tissue_type="Smooth muscle"
/cell_type="Simple columnar epithelial"
/dev_stage="Young adult"
/lab_host="XLI-BlueWRF'strain"
/clone_lib="Bos taurus Duodenum #1 library"
/notes="Organ: Intestine/Duodenum; Vector: Uni-2ZAPXR;
Site_1: EcoRI; Site_2: Xho I"

ORIGIN

Query Match 100.0%; Score 25; DB 4; Length 361;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TACCATGAGCAAAATATCATCTG 25
|||||
DB 10 TACCATGAGCAAAATATCATCTG 34

RESULT 6

LOCUS

BE589920 398 bp mRNA linear EST 27-MAR-2003
196607 BARC 5BOV Bos taurus cdna 5', mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Bos taurus (cow)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.

REFERENCE

1 (bases 1 to 398)

AUTHORS

Sonstegard, T., Capuco, A.V., White, J., Van Tassel, C.P.,
Connor, E.E., Cho, J., Sultana, R., Shade, L., Wray, J.E., Wells, K.D.
and Quackenbush, J.

TITLE

Analysis of bovine mammary gland EST and functional annotation of
the Bos taurus gene index

JOURNAL

MEDLINE

PUBMED

COMMENT

Mamm. Genome 13 (7), 373-379 (2002)

22135956

12140684

Contact: Sonstegard TS

USDA, ARS, Beltsville Agricultural Research Center

Bldg. 200 Rm 2A, Beltsville, MD 20705, USA

Tel: 301 504 8416

Fax: 301 504 8414

Email: tads@psi.barc.usda.gov

Single pass sequencing. Bases called and alt trimmed with phred

v0.980904.e. Vector identified by cross_match with the -minscore 18

and -minmatch 12 options.

PCR Primers

FORWARD: AGGAACACGATGACCAT

BACKWARD: GTTTCCCGAGTCACGACG

Plate: 118 row: F column: 21

Seq primer: ATTAGTGACACTATAG.

Location/Qualifiers

1. .398

/organism="Bos taurus"

/mol_type="mRNA"

/db_xref="taxon:9913"

/tissue_type="pooled"

/lab_host="DH10B"

/clone_lib="BARC 5BOV"

/notes="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI;
Library made from pooled mRNA isolated from mammary

tissues at eight physiological, developmental, and disease

states."

ORIGIN

Query Match 100.0%; Score 25; DB 2; Length 398;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TACCATGAGCAAAATATCATCTG 25
|||||
DB 370 TACCATGAGCAAAATATCATCTG 394

RESULT 7

LOCUS

BG688078 398 bp mRNA linear EST 27-MAR-2003
335513 BARC 5BOV Bos taurus cdna 5', mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Bos taurus (cow)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.

REFERENCE

1 (bases 1 to 398)

AUTHORS
 Sonstegard, T., Capuco, A.V., White, J., Van Tassell, C.P.,
 Connor, E.E., Cho, J., Sultana, R., Shade, L., Wray, J.E., Wells, K.D.
 and Quackenbush, J.

TITLE
 Analysis of bovine mammary gland EST and functional annotation of
 the Bos taurus gene index

JOURNAL
 Mamm. Genome 13 (7), 373-379 (2002)

MEDLINE
 22135956

PUBMED
 12140684

COMMENT
 Contact: Sonstegard TS
 USDA, ARS, Beltsville Agricultural Research Center
 Bldg. 200 Rm 2A, Beltsville, MD 20705, USA
 Tel: 301 504 8416
 Fax: 301 504 8414
 Email: tads@psi.barc.usda.gov
 Single pass sequencing. Bases called and alt trimmed with phred
 v0.980904.e. Vector identified by cross_match with the -minscore 18
 and -minmatch 12 options.
 PCR Primers
 FORWARD: AGGAACAGCTATGACCAT
 BACKWARD: GTTTCACGTCACGCG
 Plate: 34 row: I column: 18
 Seq primer: ATTTAGGTGACACTATAG.
 Location/Qualifiers
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 /organism="Bos taurus"
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 /db_xref="taxon:9913"
 /tissue_type="pooled"
 /lab_host="DH10B"
 /clone_lib="BARC 5B0V"
 /note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;
 Library made from pooled mRNA isolated from mammary
 tissues at eight physiological, developmental, and disease
 states."

FEATURES
 source
 Query Match 100.0%; Score 25; DB 4; Length 398;
 Best Local Similarity 100.0%; Pred. No. 1;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ORIGIN
 1 TACCATGAGGACAAATATCATCTG 25
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 374 TACCATGAGGACAAATATCATCTG 398

RESULT 8
 BM433056
 LOCUS 408 bp mRNA linear EST 31-JAN-2002
 DEFINITION 1JEF9D3.ab1 Bos taurus Jejenum #1 library Bos taurus cDNA, mRNA
 sequence.
 ACCESSION BM433056.1 GI:18454778
 VERSION BM433056
 KEYWORDS EST.
 SOURCE Bos taurus (cow)
 ORGANISM Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovinae; Bos.

REFERENCE
 1 (bases 1 to 408)
 Hansen, C., Fu, A., Meng, Y., Li, C., Okine, E., Senses, C.W.,
 Gordon, P.M.K. and Moore, S.S.
 Gene Expression Profiling of the Bovine Gastrointestinal Tract
 Unpublished (2002)
 Contact: Dr. Stephen Moore
 Beef Genomics Laboratory
 Dept of AFNS, University of Alberta
 410 Agri/For, Dept of AFNS, U of A, Edmonton, AB, T6G 2P5, Canada
 Tel: 780 492 0169
 Fax: 780 492 4265
 Email: stephen.moore@ualberta.ca
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 Location/Qualifiers

FEATURES
 source
 Query Match 100.0%; Score 25; DB 4; Length 408;
 Best Local Similarity 100.0%; Pred. No. 1;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ORIGIN
 1 TACCATGAGGACAAATATCATCTG 25
 |||||
 374 TACCATGAGGACAAATATCATCTG 398

RESULT 9
 BP112175
 LOCUS 411 bp mRNA linear EST 11-FEB-2003
 DEFINITION BP112175 ORCS bovine utero-placenta cDNA Bos taurus cDNA clone
 ORCS12814 5', mRNA sequence.
 ACCESSION BP112175
 VERSION BP112175.1 GI:28314465
 KEYWORDS EST.
 SOURCE Bos taurus (cow)
 ORGANISM Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovinae; Bos.

REFERENCE
 1 (bases 1 to 411)
 Ishiwata, H., Katsuma, S., Kizaki, K., Patel, O.V., Nakano, H.,
 Takahashi, T., Imai, K., Hirasawa, A., Shiojima, S., Ikawa, H.,
 Suzuki, Y., Tsujimoto, G., Izaike, Y., Todoroki, J., and Hashizume, K.
 Characterization of gene expression profiles in early bovine
 pregnancy using a custom cDNA microarray
 Mol. Reprod. Dev. 65 (1), 9-18 (2003)
 2254902
 PUBMED 12658628
 COMMENT Contact: Gozoh Tsujimoto
 Department of Molecular, Cell Pharmacology
 National Research Institute for Child Health and Development
 3-35-31 Taishido, Setagaya, Tokyo 154-8567, Japan
 Tel: 81-3-3149-2476
 Fax: 81-3-3149-1252
 Email: gtsujimoto@nch.go.jp
 This work was performed to collaborate with Developmental Biology
 Department, National Institute of Agrobiological Sciences. Address:
 2 Ikenodai, Tsukuba, Ibaraki, 305-8602 Japan. Phone & Fax:
 81-29-838-8633 e-mail: kazuha@affrc.go.jp
 This work was funded by Organized Research Combination System
 (ORCS) project of Ministry of Education, Culture, Sports, Science
 and Technology.
 Location/Qualifiers
 1..411
 /organism="Bos taurus"
 /mol_type="mRNA"
 /db_xref="taxon:9913"
 /clone="ORCS12814"
 /tissue_type="mixture of uterus and placenta"
 /dev_stage="adult"
 /clone_lib="ORCS bovine utero-placenta cDNA"

ORIGIN
 Query Match 100.0%; Score 25; DB 5; Length 411;
 Best Local Similarity 100.0%; Pred. No. 1;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

source
 1..408
 /organism="Bos taurus"
 /mol_type="mRNA"
 /db_xref="taxon:9913"
 /tissue_type="Smooth muscle"
 /cell_type="Simple columnar epithelial"
 /dev_stage="Young adult"
 /lab_host="XLI-BlueMFP, strain"
 /clone_lib="Bos taurus Jejenum #1 library"
 /note="Organ: Intestine/Jejunum; Vector: Uni-2ZAPXR;
 Site_1: EcoRI; Site_2: Xho I"

ORIGIN
 Query Match 100.0%; Score 25; DB 4; Length 408;
 Best Local Similarity 100.0%; Pred. No. 1;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY
 1 TACCATGAGGACAAATATCATCTG 25
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 330 TACCATGAGGACAAATATCATCTG 354

Db
 330 TACCATGAGGACAAATATCATCTG 354

RESULT 9
 BP112175
 LOCUS 411 bp mRNA linear EST 11-FEB-2003
 DEFINITION BP112175 ORCS bovine utero-placenta cDNA Bos taurus cDNA clone
 ORCS12814 5', mRNA sequence.
 ACCESSION BP112175
 VERSION BP112175.1 GI:28314465
 KEYWORDS EST.
 SOURCE Bos taurus (cow)
 ORGANISM Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovinae; Bos.

REFERENCE
 1 (bases 1 to 411)
 Ishiwata, H., Katsuma, S., Kizaki, K., Patel, O.V., Nakano, H.,
 Takahashi, T., Imai, K., Hirasawa, A., Shiojima, S., Ikawa, H.,
 Suzuki, Y., Tsujimoto, G., Izaike, Y., Todoroki, J., and Hashizume, K.
 Characterization of gene expression profiles in early bovine
 pregnancy using a custom cDNA microarray
 Mol. Reprod. Dev. 65 (1), 9-18 (2003)
 2254902
 PUBMED 12658628
 COMMENT Contact: Gozoh Tsujimoto
 Department of Molecular, Cell Pharmacology
 National Research Institute for Child Health and Development
 3-35-31 Taishido, Setagaya, Tokyo 154-8567, Japan
 Tel: 81-3-3149-2476
 Fax: 81-3-3149-1252
 Email: gtsujimoto@nch.go.jp
 This work was performed to collaborate with Developmental Biology
 Department, National Institute of Agrobiological Sciences. Address:
 2 Ikenodai, Tsukuba, Ibaraki, 305-8602 Japan. Phone & Fax:
 81-29-838-8633 e-mail: kazuha@affrc.go.jp
 This work was funded by Organized Research Combination System
 (ORCS) project of Ministry of Education, Culture, Sports, Science
 and Technology.
 Location/Qualifiers
 1..411
 /organism="Bos taurus"
 /mol_type="mRNA"
 /db_xref="taxon:9913"
 /clone="ORCS12814"
 /tissue_type="mixture of uterus and placenta"
 /dev_stage="adult"
 /clone_lib="ORCS bovine utero-placenta cDNA"

FEATURES
 source
 1..411
 /organism="Bos taurus"
 /mol_type="mRNA"
 /db_xref="taxon:9913"
 /clone="ORCS12814"
 /tissue_type="mixture of uterus and placenta"
 /dev_stage="adult"
 /clone_lib="ORCS bovine utero-placenta cDNA"

ORIGIN
 Query Match 100.0%; Score 25; DB 5; Length 411;
 Best Local Similarity 100.0%; Pred. No. 1;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TACCATGAGGACAAATATCATCTG 25
 |||||
 Db 386 TACCATGAGGACAAATATCATCTG 410
 |||||

RESULT 10
 BM433038

LOCUS
 DEFINITION 413 bp mRNA linear EST 31-JAN-2002
 LJEU9B6.ab1 Bos taurus Jejenum #1 library Bos taurus cDNA, mRNA
 sequence.

ACCESSION
 BM433038
 VERSION BM433038.1 GI:18454760
 KEYWORDS
 EST.
 SOURCE Bos taurus (cow)
 ORGANISM Bos taurus

REFERENCE
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovinae; Bos.
 1 (bases 1 to 413)
 Hansen, C., Fu, A., Meng, Y., Li, C., Okine, E., Sensen, C.W.,
 Gordon, P.M.K. and Moore, S.S.
 Gene Expression Profiling of the Bovine Gastrointestinal Tract
 Unpublished (2002)

TITLE
 JOURNAL
 COMMENT Contact: Dr. Stephen Moore
 Beef Genomics Laboratory
 Dept of AFNS, University of Alberta
 410 Agri/For, Dept of AFNS, U of A, Edmonton, AB, T6G 2P5, Canada
 Tel: 780 492 0169
 Fax: 780 492 4265
 Email: stephen.moore@ualberta.ca
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FEATURES
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 /mol_type="mRNA"
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 /cell_type="Simple columnar epithelial"
 /dev_stage="Young adult"
 /lab_host="XLI-BlueMRF" strain"
 /clone_lib="Bos taurus Jejenum #1 library"
 /notes="Organ: Intestine/Jejunum; Vector: Uni-2ZAPXR;
 Site_1: EcoRI; Site_2: Xho I"

ORIGIN
 Query Match 100.0%; Score 25; DB 4; Length 413;
 Best Local Similarity 100.0%; Pred. No. 1;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TACCATGAGGACAAATATCATCTG 25
 |||||
 Db 372 TACCATGAGGACAAATATCATCTG 396
 |||||

RESULT 11
 CB225030

LOCUS
 DEFINITION 414 bp mRNA linear EST 10-FEB-2003
 10M28B03 Bos taurus Omasum #1 library Bos taurus cDNA, mRNA
 sequence.

ACCESSION
 CB225030
 VERSION CB225030.1 GI:28295544
 KEYWORDS
 EST.
 SOURCE Bos taurus (cow)
 ORGANISM Bos taurus

REFERENCE
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovinae; Bos.
 1 (bases 1 to 414)
 Hansen, C., Fu, A., Meng, Y., Li, C., Okine, E., Sensen, C.W.,
 Gordon, P.M.K. and Moore, S.S.
 Gene Expression Profiling of the Bovine Gastrointestinal Tract
 Unpublished (2002)

COMMENT Contact: Dr. Stephen Moore
 Beef Genomics Laboratory
 Dept of AFNS, University of Alberta
 410 Agri/For, Dept of AFNS, U of A, Edmonton, AB, T6G 2P5, Canada
 Tel: 780 492 0169
 Fax: 780 492 4265
 Email: stephen.moore@ualberta.ca
 Insert Length: 414 Std Error: 0.00
 POLYA=Yes.

FEATURES
 source Location/Qualifiers
 1..414
 /organism="Bos taurus"
 /mol_type="mRNA"
 /db_xref="taxon:9913"
 /tissue_type="Smooth muscle"
 /cell_type="Stratified squamous epithelial"
 /dev_stage="Young adult"
 /lab_host="XLI-BlueMRF" strain"
 /clone_lib="Bos taurus Omasum #1 library"
 /notes="Organ: Omasum; Vector: Uni-2ZAPXR; Site_1: EcoRI;
 Site_2: Xho I"

ORIGIN
 Query Match 100.0%; Score 25; DB 6; Length 414;
 Best Local Similarity 100.0%; Pred. No. 1;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TACCATGAGGACAAATATCATCTG 25
 |||||
 Db 183 TACCATGAGGACAAATATCATCTG 207
 |||||

RESULT 12
 BP110134

LOCUS
 DEFINITION 431 bp mRNA linear EST 11-FEB-2003
 BP110134 ORCS bovine utero-placenta cDNA Bos taurus cDNA clone
 ORCS10131 5', mRNA sequence.

ACCESSION
 BP110134
 VERSION BP110134.1 GI:28312422
 KEYWORDS
 EST.
 SOURCE Bos taurus (cow)
 ORGANISM Bos taurus

REFERENCE
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovinae; Bos.
 1 (bases 1 to 431)
 Ishiwata, H., Katsuma, S., Kizaki, K., Patel, O.V., Nakano, H.,
 Takahashi, T., Imai, K., Hirasawa, A., Shiojima, S., Ikawa, H.,
 Suzuki, Y., Tsujimoto, G., Izaike, Y., Todoroki, J. and Hashizume, K.
 Characterization of gene expression profiles in early bovine
 pregnancy using a custom cDNA microarray
 Mol. Reprod. Dev. 65 (1), 9-18 (2003)
 22544902
 12658628

JOURNAL
 MEDLINE
 PUBMED
 COMMENT Contact: Gozoh Tsujimoto
 Department of Molecular, Cell Pharmacology
 National Research Institute for Child Health and Development
 3-35-31 Taishido, Setagaya, Tokyo 154-8567, Japan
 Tel: 81-3-3149-2476
 Fax: 81-3-3149-1252
 Email: gtsujimoto@nch.go.jp
 This work was performed to collaborate with Developmental Biology
 Department, National Institute of Agrobiological Sciences. Address:
 2 Ikenodai, Tsukuba, Ibaraki, 305-8602 Japan. Phone & Fax:
 81-29-838-8633 e-mail: kazuna@affrc.go.jp
 This work was funded by Organized Research Combination System
 (ORCS) project of Ministry of Education, Culture, Sports, Science
 and Technology.

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 source Location/Qualifiers
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 /organism="Bos taurus"
 /mol_type="mRNA"
 /db_xref="taxon:9913"

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/dev_stage="adult"
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Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 373 TACCATGAGGACAAATATCATCTG 397

RESULT 13
AV613710
LOCUS
DEFINITION AV613710 Bos taurus adipocyte cell line Bos taurus cDNA clone
E0AD009D01 5', mRNA sequence.
ACCESSION AV613710
VERSION AV613710.1 GI:9749380
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
REFERENCE 1 (bases 1 to 432)
AUTHORS Takasuga,A., Hirotsune,S., Itoh,R., Jitohzono,A., Suzuki,H., Aso,H.
and Sugimoto,Y.
TITLE Establishment of a high throughput EST sequencing system using
poly(A) tail-removed cDNA libraries and determination of 36,000
bovine ESTs
JOURNAL Nucleic Acids Res. 29 (22), E108 (2001)
MEDLINE 21570554
PUBMED 11713328
COMMENT Contact: Yoshikazu Sugimoto
Animal Genetics Division
Shirakawa Institute of Animal Genetics
Odakura, Nishigo, Nishi-shirakawa, Fukushima 961-8061, Japan
Tel: 81-248-25-5641
Fax: 81-248-25-5725
Email: kazusugi@cococ.ocn.ne.jp
Single pass sequencing.
This clone was obtained from a polyA-deleted cDNA library.
FEATURES
source
Location/Qualifiers
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/organism="Bos taurus"
/mol_type="mRNA"
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/clone="EIBR035A07"
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/dev_stage="fetus"
/lab_host="DH10B"
/clone_lib="Bos taurus brain fetus"
/notes="Vector: pZLI; Site 1: SalI; Site 2: NotI; Poly A
was deleted from a NotI site"

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Query Match      100.0%; Score 25; DB 1; Length 432;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TACCATGAGGACAAATATCATCTG 25
    |||||
Db 65 TACCATGAGGACAAATATCATCTG 41

RESULT 15
CB060174
LOCUS
DEFINITION CB060174 BARC-EMBRAPA 326BOV Bos indicus cDNA clone 326BOV_1023
Unknown, mRNA sequence.
ACCESSION CB060174
VERSION CB060174.1 GI:27798461
KEYWORDS EST.
SOURCE Bos indicus (zebu)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
REFERENCE 1 (bases 1 to 436)
AUTHORS da Mota,A.F., Sonstegard,T.S., Van Tassell,C.P., Matukumalli,L.K.,
Wood,B.L., Capuco,A.V., Brito,M.A.P., Martinez,M.L., Connor,E.E.,
Machado,M.A. and Coutinho,L.L.
TITLE Construction and Characterization of cDNA Libraries Generated from
Mammary Gland Tissues of Holstein (Bos taurus) and Gir (Bos
indicus) Cattle
JOURNAL Unpublished (2002)
COMMENT Contact: Adilson F. da Mota
Gene Evaluation and Mapping Laboratory
USDA, ARS, Animal and Natural Resources Institute
Bldg. 200 Rm3 BARC-East, Beltsville, MD 20705, USA

```

Tel: 3015048456
Fax: 3015048414
Email: amota@cnpg1.embrapa.br
Single pass sequencing. Bases called and trimmed with phred
0.000925 using options -trim alt '' -trim fasta. Vector identified
by cross match using options -mismatch 12 -minscore 12
PCR PRIMERS
FORWARD: GTTTCCTCCAGTCACGACGTTG
BACKWARD: TGACGGGATACAAATTCACACAG
Plate: 1 row: 0 column: 23
Seq primer: GTTTCCTCCAGTCACGACGTTG
High quality sequence stop: 436.
Location/Qualifiers

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/strain="Brazilian Dairy Gir"
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/clone="326BOV_1023"
/sex="female"
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/cell_type="epithelium"
/dev_stage="involutus"
/lab_host="DH5alpha"
/clone_lib="BARC-EMBRAPA 326BOV"
/note="Organ: mammary; Vector: pUC 118; Site 1: HincII;
Site 2: HincII; This mammary-derived cDNA library was
created as part of a collaborative project between the ARS
Gene Evaluation and Mapping Laboratory and the EMBRAPA
Dairy Cattle Research Center under the sponsorship of
USDA, ARS/EMBRAPA-LABEX program in animal genomics. RNA
sample from cow AML, samples 2, 4, and 5 extracted on
3/27/02, RT with Superscript II at 37 deg C annealing
temperature, PCR with 16-mers."

ORIGIN

Query Match 100.0%; Score 25; DB 6; Length 436;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 342 TACCATGAGGACAAATATCATCTCTG 366

Search completed: November 17, 2004, 02:10:47
Job time : 349.642 secs

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RESULT 2
US-09-960-352-6557
; Sequence 6557, Application US/09960352
; Patent No. US20020137139A1

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; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 6557
; LENGTH: 346
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 28-LIB34-007-Q1-E1-G7
US-09-960-352-6557

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Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TACCATGAGGACAAATATCATCTG 25
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Db 174 TACCATGAGGACAAATATCATCTG 198

RESULT 3
US-09-960-352-6350
; Sequence 6350, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 6350
; LENGTH: 353
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 27-LIB34-033-Q1-E1-G3
US-09-960-352-6350

Query Match      100.0%; Score 25; DB 9; Length 353;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TACCATGAGGACAAATATCATCTG 25
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Db 324 TACCATGAGGACAAATATCATCTG 348

RESULT 4
US-09-960-352-7247
; Sequence 7247, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
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; SEQ ID NO 7247
; LENGTH: 380
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 31-LIB34-008-Q1-E1-H11
US-09-960-352-7247

Query Match      100.0%; Score 25; DB 9; Length 380;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TACCATGAGGACAAATATCATCTG 25
    |||||
Db 174 TACCATGAGGACAAATATCATCTG 198

RESULT 5
US-09-960-352-1396
; Sequence 1396, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 1396
; LENGTH: 388
; TYPE: DNA
; ORGANISM: Bos taurus
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (44),(60)
; OTHER INFORMATION: unsure at all n locations
; OTHER INFORMATION: Clone ID: 07-BOVMS1-018-Q1-E1-B3
US-09-960-352-1396

Query Match      100.0%; Score 25; DB 9; Length 388;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TACCATGAGGACAAATATCATCTG 25
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Db 103 TACCATGAGGACAAATATCATCTG 133

RESULT 6
US-09-960-352-7805
; Sequence 7805, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 7805
; LENGTH: 397
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 34-BOVMS1-002-Q1-E1-A6
US-09-960-352-7805
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Best Local Similarity 100.0%; Pred. No. 0.2;
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Db 125 TACCATGAGGACAAATATCATCTG 149

RESULT 7
US-09-960-352-12218
; Sequence 12218, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 12218
; LENGTH: 402
; TYPE: DNA
; ORGANISM: Bos taurus
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (300)
; OTHER INFORMATION: unsure at all n locations
; OTHER INFORMATION: Clone ID: 52-LIB34-007-Q1-E1-E8
US-09-960-352-12218

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Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 309 TACCATGAGGACAAATATCATCTG 333

RESULT 8
US-09-960-352-4672
; Sequence 4672, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 4672
; LENGTH: 409
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 20-LIB34-031-Q1-E1-E7
US-09-960-352-4672

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Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TACCATGAGGACAAATATCATCTG 25
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Db 340 TACCATGAGGACAAATATCATCTG 364

RESULT 9
US-09-960-352-7414
; Sequence 7414, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 7414
; LENGTH: 409
; TYPE: DNA
; ORGANISM: Bos taurus
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (300)
; OTHER INFORMATION: unsure at all n locations
; OTHER INFORMATION: Clone ID: 32-LIB3057-021-Q1-K1-H7
US-09-960-352-7414

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Best Local Similarity 100.0%; Pred. No. 0.2;
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Db 373 TACCATGAGGACAAATATCATCTG 397

RESULT 10
US-09-960-352-9374
; Sequence 9374, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 9374
; LENGTH: 409
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 40-LIB34-028-Q1-E1-B12
US-09-960-352-9374

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QY 1 TACCATGAGGACAAATATCATCTG 25
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Db 379 TACCATGAGGACAAATATCATCTG 403

RESULT 11
US-09-960-352-8498
; Sequence 8498, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
```

; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 8498
; LENGTH: 411
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 36-LIB34-071-Q1-E1-A8
US-09-960-352-8498

Query Match 100.0%; Score 25; DB 9; Length 411;
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Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TACCATGAGGACAAATATCATCTG 25
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Db 378 TACCATGAGGACAAATATCATCTG 402

RESULT 12

US-09-960-352-1120
; Sequence 1120, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:

; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan

; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 1120
; LENGTH: 412
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 05-LIB34-063-Q1-E1-B1
US-09-960-352-1120

Query Match 100.0%; Score 25; DB 9; Length 412;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TACCATGAGGACAAATATCATCTG 25
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Db 372 TACCATGAGGACAAATATCATCTG 396

RESULT 13

US-09-960-352-2257
; Sequence 2257, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:

; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan

; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 2257
; LENGTH: 413
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 10-LIB34-017-Q1-E1-C5

US-09-960-352-2257

Query Match 100.0%; Score 25; DB 9; Length 413;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TACCATGAGGACAAATATCATCTG 25
|||||
Db 384 TACCATGAGGACAAATATCATCTG 408

RESULT 14

US-09-960-352-11264
; Sequence 11264, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:

; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan

; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 11264
; LENGTH: 414
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 48-LIB34-026-Q1-E1-D8
US-09-960-352-11264

Query Match 100.0%; Score 25; DB 9; Length 414;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TACCATGAGGACAAATATCATCTG 25
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Db 384 TACCATGAGGACAAATATCATCTG 408

RESULT 15

US-09-960-352-5186
; Sequence 5186, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:

; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan

; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 5186
; LENGTH: 415
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 22-LIB34-073-Q1-E1-F5
US-09-960-352-5186

Query Match 100.0%; Score 25; DB 9; Length 415;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TACCATGAGGACAAATATCATCTG 25
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Db 374 TACCATGAGGACAAATATCATCTG 398

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Job time : 39.2849 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 16, 2004, 16:25:24 ; Search time 769.82 Seconds
(without alignments)
3218.578 Million cell updates/sec

Title: US-09-821-782E-48

Perfect score: 472

Sequence: 1 taccatgagacaatatct.....attcctaacaactaggagg 472

Scoring table: IDENTITY_NUC

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Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: Geneseqn1990s:*
3: Geneseqn2000s:*
4: Geneseqn2001as:*
5: Geneseqn2001bs:*
6: Geneseqn2002as:*
7: Geneseqn2002bs:*
8: Geneseqn2003as:*
9: Geneseqn2003bs:*
10: Geneseqn2003cs:*
11: Geneseqn2003ds:*
12: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	392	83.1	472	8	ABQ83308
3	387.2	82.0	472	8	ABQ83307
4	384	81.4	472	8	ABQ83306
5	384	81.4	472	8	ABQ83321
6	376	79.7	472	8	ABQ83333
7	374.4	79.3	472	8	ABQ83331
8	374.4	79.3	472	8	ABQ83334
9	372.8	79.0	472	8	ABQ83303
10	372.8	79.0	472	8	ABQ83330
11	371.8	78.8	472	8	ABQ83311
12	371.2	78.6	472	8	ABQ83313
13	371.2	78.6	472	8	ABQ83332
14	371.2	78.6	472	8	ABQ83328
15	369.6	78.3	472	8	ABQ83310
16	369.6	78.3	472	8	ABQ83315
17	369.6	78.3	472	8	ABQ83304
18	369.6	78.3	472	8	ABQ83326
19	368	78.0	472	8	ABQ83314
20	368	78.0	472	8	ABQ83322
21	368	78.0	472	8	ABQ83312

22	368	78.0	472	8	ABQ83337	Abq83337 Mitochond
23	367.2	77.8	472	8	ABQ83301	Abq83301 Mitochond
24	365.6	77.5	472	8	ABQ83317	Abq83317 Mitochond
25	364.8	77.3	472	8	ABQ83336	Abq83336 Mitochond
26	364.8	77.3	472	8	ABQ83335	Abq83335 Mitochond
27	363.2	76.9	472	8	ABQ83320	Abq83320 Mitochond
28	361.6	76.6	472	8	ABQ83327	Abq83327 Mitochond
29	361.6	76.6	472	8	ABQ83309	Abq83309 Mitochond
30	361.6	76.6	472	8	ABQ83338	Abq83338 Mitochond
31	360	76.3	472	8	ABQ83319	Abq83319 Mitochond
32	360	76.3	472	8	ABQ83305	Abq83305 Mitochond
33	358.4	75.9	472	8	ABQ83323	Abq83323 Mitochond
34	358.4	75.9	472	8	ABQ83316	Abq83316 Mitochond
35	356.8	75.6	472	8	ABQ83340	Abq83340 Mitochond
36	355.2	75.3	472	8	ABQ83339	Abq83339 Mitochond
37	354.8	75.2	472	8	ABQ83302	Abq83302 Mitochond
38	351.4	74.4	472	8	ABQ83329	Abq83329 Mitochond
39	350	74.2	472	8	ABQ83324	Abq83324 Mitochond
40	347.2	73.6	472	8	ABQ83318	Abq83318 Mitochond
41	345.2	73.1	472	8	ABQ83325	Abq83325 Mitochond
42	321.6	68.1	1144	10	ADB35253	Add5253 Mouse mlt
43	321.6	68.1	3552	2	AAZ77492	Aaz77492 Human ova
44	320	67.8	599	3	AAC86457	Aac86457 Mouse cyt
45	318.4	67.5	16300	10	ADB59175	Adb59175 Toxicity-

ALIGNMENTS

RESULT 1
ABQ83296
ID ABQ83296 standard; DNA; 472 BP.
XX
AC ABQ83296;
XX
DT 18-JAN-2003 (first entry)
XX
DE Antelope cervicapra mitochondrial cytochrome b gene SEQ ID NO:1.
XX
KW Mitochondrial cytochrome b gene; mitochondrial; cytochrome b;
KW identification; criminal investigation; animal poaching;
KW Antelope cervicapra; blackbuck; gene; ds.
XX
OS Antelope cervicapra.
XX
PN WO200277278-A1.
XX
PD 03-OCT-2002.
XX
PF 28-MAR-2001; 2001WO-IN000055.
XX
PR 28-MAR-2001; 2001WO-IN000055.
XX
(COUL) COUNCIL SCI & IND RES.
XX
Verma SK, Singh L;
XX
WPI; 2003-018945/01.
XX
New universal primers, mcb 398 and mcb 869, capable of amplifying a
fragment of cytochrome b gene of any animal species, useful for
establishing the identity of biological materials and animals for
molecular evidence in forensics.
XX
Claim 5; Page 116; 128pp; English.
XX
The present invention describes universal primers, mcb 398 and mcb 869
(see ABQ83297 and ABQ83298), capable of amplifying a fragment of
cytochrome b gene of any animal species in polymerase chain reaction
of unknown origin at species and sub-species level. Also described is a
method for the identification of the animal from a biological sample. The
method is used for animal identification to establish the crime with the

CC criminal beyond a reasonable doubt, to establish the identity of
 CC biological materials such as skin, horns confiscated from animal
 CC poachers, if it is that of an endangered species, for the purpose of
 CC molecular evidence of animal hunting and related crime in the court of
 CC law, so that human violation of the wildlife resources could be
 CC controlled, to have an idea of the geographical location of the
 CC commitment of wildlife crime based on the cytochrome b gene haplotype of
 CC poached animal identified by the universal primer invented, to detect the
 CC adulteration of animal meat in food products for the purpose of food
 CC fortification, by the food fortification agencies, to provide a universal
 CC technique for detection of the origin of blood or blood stains collected
 CC from the scene of the crime related to offenses such as murder and rape,
 CC in order to establish the origin of blood found at the scene of the crime
 CC when it sounds as if criminals intentionally spread the blood of an
 CC animal at the scene of the crime to confuse the crime investigators and
 CC forensic scientists with human blood, and so that the method can be
 CC converted to a commercial molecular kit and DNA chips based applications
 CC for wildlife identification in forensics. The present sequence represents
 CC a specifically claimed Antelope cervicapra (blackbuck) mitochondrial
 CC cytochrome b gene sequence from the present invention
 XX
 SQ Sequence 472 BP; 146 A; 145 C; 61 G; 120 T; 0 U; 0 Other;

Query Match 100.0%; Score 472; DB 8; Length 472;
 Best Local Similarity 100.0%; Pred. No. 1.5e-137;
 Matches 472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TACCATGAGGACAAATATCTTTTTCAGGAGCAACAGTATCATCAACCAATCTCTTTTCAGCAA 60
 Db 1 TACCATGAGGACAAATATCTTTTTCAGGAGCAACAGTATCATCAACCAATCTCTTTTCAGCAA 60

Qy 61 TCCCATATACCGTACAAACCTAGTAGATGAATCTGAGGAGGTTCTCAGTAGATAAG 120
 Db 61 TCCCATATACCGTACAAACCTAGTAGATGAATCTGAGGAGGTTCTCAGTAGATAAG 120

Qy 121 CAACCTTTACCGGATTTTTCGCTTCCACTTTATCTCCATTTATCATTTGAGGCCCTTA 180
 Db 121 CAACCTTTACCGGATTTTTCGCTTCCACTTTATCTCCATTTATCATTTGAGGCCCTTA 180

Qy 181 CCATAGTACACCTACTGTGTTTTCACGAAACAGGATCCAAACCCCAAGGAATCTCAT 240
 Db 181 CCATAGTACACCTACTGTGTTTTCACGAAACAGGATCCAAACCCCAAGGAATCTCAT 240

Qy 241 CAGACGACAGCAAAATTCATTTCCACCCCTACTACACTATCAAGATATCTTAGAGCTC 300
 Db 241 CAGACGACAGCAAAATTCATTTCCACCCCTACTACACTATCAAGATATCTTAGAGCTC 300

Qy 301 TACTATTAAATTTAAACCCCTCATGCTTCTAGTCTTATCTTCCCGGACCTGCTTGGAGACC 360
 Db 301 TACTATTAAATTTAAACCCCTCATGCTTCTAGTCTTATCTTCCCGGACCTGCTTGGAGACC 360

Qy 361 CAGACAACTATACACAGCAAAACCCCACTTAATACACCCCAATATCAAGCCCGAATGAT 420
 Db 361 CAGACAACTATACACAGCAAAACCCCACTTAATACACCCCAATATCAAGCCCGAATGAT 420

Qy 421 ACTTCCTATTTCATACGCAATCTTCCGATCAATTTCTTAACAACTAGGAGG 472
 Db 421 ACTTCCTATTTCATACGCAATCTTCCGATCAATTTCTTAACAACTAGGAGG 472

RESULT 2
 ABQ83308
 ID ABQ83308 standard; DNA; 472 BP.
 XX
 AC ABQ83308;
 XX
 DT 18-JAN-2003 (first entry)
 XX
 DE Mitochondrial cytochrome b gene sequence SEQ ID NO:13.
 XX
 KW Mitochondrial cytochrome b gene; mitochondrial; cytochrome b;
 KW identification; criminal investigation; animal poaching; gene; ds.
 XX

OS Unidentified.
 XX WO200277278-A1.
 XX 03-OCT-2002.
 XX 28-MAR-2001; 2001WO-IN000055.
 XX 28-MAR-2001; 2001WO-IN000055.
 XX (COUL) COUNCIL SCI & IND RES.
 XX Verma SK, Singh L;
 XX WPI; 2003-018945/01.
 XX New universal primers, mcb 398 and mcb 869, capable of amplifying a
 XX fragment of cytochrome b gene of any animal species, useful for
 XX establishing the identity of biological materials and animals for
 XX molecular evidence in forensics.
 XX Example 1; Page 28-57; 128pp; English.
 XX The present invention describes universal primers, mcb 398 and mcb 869
 XX (see ABQ83297 and ABQ83298), capable of amplifying a fragment of
 XX cytochrome b gene of any animal species in polymerase chain reaction
 XX (PCR) and revealing the identity of the biological material of any animal
 XX of unknown origin at species and sub-species level. Also described is a
 XX method for the identification of the animal from a biological sample. The
 XX method is used for animal identification to establish the crime with the
 XX criminal beyond a reasonable doubt, to establish the identity of
 XX biological materials such as skin, horns confiscated from animal
 XX poachers, if it is that of an endangered species, for the purpose of
 XX molecular evidence of animal hunting and related crime in the court of
 XX law, so that human violation of the wildlife resources could be
 XX controlled, to have an idea of the geographical location of the
 XX poached animal identified by the universal primer invented, to detect the
 XX adulteration of animal meat in food products for the purpose of food
 XX fortification, by the food fortification agencies, to provide a universal
 XX technique for detection of the origin of blood or blood stains collected
 XX from the scene of the crime related to offenses such as murder and rape,
 XX in order to establish the origin of blood found at the scene of the crime
 XX when it sounds as if criminals intentionally spread the blood of an
 XX animal at the scene of the crime to confuse the crime investigators and
 XX forensic scientists with human blood, and so that the method can be
 XX converted to a commercial molecular kit and DNA chips based applications
 XX for wildlife identification in forensics. The present sequence represents
 XX a mitochondrial cytochrome b gene sequence from the present invention
 XX
 SQ Sequence 472 BP; 143 A; 153 C; 60 G; 116 T; 0 U; 0 Other;

Query Match 83.1%; Score 392; DB 8; Length 472;
 Best Local Similarity 89.4%; Pred. No. 1.9e-112;
 Matches 422; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

Qy 1 TACCATGAGGACAAATATCTTTTTCAGGAGCAACAGTATCATCAACCAATCTCTTTTCAGCAA 60
 Db 1 TCCCATATGAGGACAAATATCTTTTTCAGGAGCAACAGTATCATCAACCAATCTCTTTTCAGCAA 60

Qy 61 TCCCATATACCGTACAAACCTAGTAGATGAATCTGAGGAGGTTCTCAGTAGATAAG 120
 Db 61 TCCCATATATGAGTACAAACCTAGTAGATGAATCTGAGGAGGTTCTCAGTAGATAAG 120

Qy 121 CAACCTTTACCGGATTTTTCGCTTCCACTTTATCTCCATTTATCATTTGAGGCCCTTA 180
 Db 121 CAACCTTTACCGGATTTTTCGCTTCCACTTTATCTCCATTTATCATTTGAGGCCCTTA 180

Qy 181 CCATAGTACACCTACTGTGTTTTCACGAAACAGGATCCAAACCCCAAGGAATCTCAT 240
 Db 181 CCATAGTACACCTACTGTGTTTTCACGAAACAGGATCCAAACCCCAAGGAATCTCAT 240

Qy 241 CAGACGACAGCAAAATTCATTTCCACCCCTACTACACTATCAAGATATCTTAGAGCTC 300
 Db 241 CAGACGACAGCAAAATTCATTTCCACCCCTACTACACTATCAAGATATCTTAGAGCTC 300

Qy 301 TACTATTAAATTTAAACCCCTCATGCTTCTAGTCTTATCTTCCCGGACCTGCTTGGAGACC 360
 Db 301 TACTATTAAATTTAAACCCCTCATGCTTCTAGTCTTATCTTCCCGGACCTGCTTGGAGACC 360

Qy 361 CAGACAACTATACACAGCAAAACCCCACTTAATACACCCCAATATCAAGCCCGAATGAT 420
 Db 361 CAGACAACTATACACAGCAAAACCCCACTTAATACACCCCAATATCAAGCCCGAATGAT 420

Qy 421 ACTTCCTATTTCATACGCAATCTTCCGATCAATTTCTTAACAACTAGGAGG 472
 Db 421 ACTTCCTATTTCATACGCAATCTTCCGATCAATTTCTTAACAACTAGGAGG 472

XX New universal primers, mcb 398 and mcb 869, capable of amplifying a
PT fragment of cytochrome b gene of any animal species, useful for
PT establishing the identity of biological materials and animals for
PT molecular evidence in forensics.

XX
XX
XX Example 1; Page 28-57; 128pp; English.

XX The present invention describes universal primers, mcb 398 and mcb 869
CC (see ABQ83297 and ABQ83298), capable of amplifying a fragment of
CC cytochrome b gene of any animal species in polymerase chain reaction
CC (PCR) and revealing the identity of the biological material of any animal
CC of unknown origin at species and sub-species level. Also described is a
CC method for the identification of the animal from a biological sample. The
CC method is used for animal identification to establish the crime with the
CC criminal beyond a reasonable doubt, to establish the identity of
CC biological materials such as skin, horns confiscated from animal
CC poachers, if it is that of an endangered species, for the purpose of
CC molecular evidence of animal hunting and related crime in the court of
CC law, so that human violation of the wildlife resources could be
CC controlled, to have an idea of the geographical location of the
CC commitment of wildlife crime based on the cytochrome b gene haplotype of
CC poached animal identified by the universal primer invented, to detect the
CC adulteration of animal meat in food products for the purpose of food
CC fortification, by the food fortification agencies, to provide a universal
CC technique for detection of the origin of blood or blood stains collected
CC from the scene of the crime related to offenses such as murder and rape,
CC in order to establish the origin of blood found at the scene of the crime
CC when it sounds as if criminals intentionally spread the blood of an
CC animal at the scene of the crime to confuse the crime investigators and
CC forensic scientists with human blood, and so that the method can be
CC converted to a commercial molecular kit and DNA chips based applications
CC for wildlife identification in forensics. The present sequence represents
CC a mitochondrial cytochrome b gene sequence from the present invention

XX
XX
XX Sequence 472 BP; 140 A; 153 C; 66 G; 113 T; 0 U; 0 Other;

Query Match 81.4%; Score 384; DB 8; Length 472;
Best Local Similarity 88.3%; Pred. No. 6.1e-110;
Matches 417; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

Qy 1 TACCATGAGGACAAATATCTTTTGGAGGACAAAGTCATCACCACATCTCTCTTCAGCAA 60
Db 1 TCCCATATATGGCAGACACCTAGTAATGAATCTGAGGGGCAACAGTCATCACCACATCTCTCTTCAGCAA 60

Qy 61 TCCCATATATGGCAGACACCTAGTAATGAATCTGAGGGGCAACAGTCATCACCACATCTCTCTTCAGCAA 120
Db 61 TCCCATATATGGCAGACACCTAGTAATGAATCTGAGGGGCAACAGTCATCACCACATCTCTCTTCAGCAA 120

Qy 121 CAACCCCTTACCCGATTTTTCGCTTCCACTTTATCTCCCAATTTATCATTCGACGCCCTTA 180
Db 121 CAACCCCTTACCCGATTTTTCGCTTCCACTTTATCTCCCAATTTATCATTCGACGCCCTTG 180

Qy 181 CCATAGTACCTACTGTTTCTCCAGAAACAGGATCCAAACCCACAGGAATCTCAT 240
Db 181 CCATAGTACCTACTGTTTCTCCAGAAACAGGATCCAAACCCACAGGAATCTCAT 240

Qy 241 CAGACGAGACAAATATCCATTCACCCCTACTACATTCAGATATCTAGAGCTC 300
Db 241 CAGACGAGATATAATCCCATTCACCCCTACTATACATCAAGGACATCTAGGCGCC 300

Qy 301 TACTATTAATTTAAACCCCTCATGTTCTTAGTCTCTTATCTTCAACCGGACCTGTTGGAGACC 360
Db 301 TATTACTAATCTAGCCCTCATACTACTAGTACTATTTCGACCCGACCTGCTGGAGACC 360

Qy 361 CAGACACTATACACGAGCAACCCACTTATATACACCCCAATATCAAGCCCAATGAT 420
Db 361 CAGACACTATACACCCGCAACCCACTTATATACACCCCAATATCAAGCCCAATGAT 420

Qy 421 ACTTCCTATTGTGATAGGCAATCTCCGATCAATTTCTTAACAAACTAGGAGG 472
Db 421 ATTTCCTATTGTGATAGGCAATCTCCGATCAATTTCTTAACAAACTAGGAGG 472

RESULT 5
ABQ83321
ID ABQ83321 standard; DNA; 472 BP.

XX
XX AC ABQ83321;

XX
XX DT 18-JAN-2003 (first entry)

XX
XX DE Mitochondrial cytochrome b gene sequence SEQ ID NO:26.

XX
XX KW Mitochondrial cytochrome b gene; mitochondrial; cytochrome b;
XX identification; criminal investigation; animal poaching; gene; ds.

XX
XX OS Unidentified.

XX
XX PN WO200277278-A1.

XX
XX PD 03-OCT-2002.

XX
XX PF 28-MAR-2001; 2001WO-IN000055.

XX
XX PR 28-MAR-2001; 2001WO-IN000055.

XX
XX PA (COUL) COUNCIL SCI & IND RES.

XX
XX PI Verma SK, Singh L;

XX
XX WPI; 2003-018945/01.

XX
XX New universal primers, mcb 398 and mcb 869, capable of amplifying a
XX fragment of cytochrome b gene of any animal species, useful for
XX establishing the identity of biological materials and animals for
XX molecular evidence in forensics.

XX
XX Example 1; Page 28-57; 128pp; English.

XX The present invention describes universal primers, mcb 398 and mcb 869
CC (see ABQ83297 and ABQ83298), capable of amplifying a fragment of
CC cytochrome b gene of any animal species in polymerase chain reaction
CC (PCR) and revealing the identity of the biological material of any animal
CC of unknown origin at species and sub-species level. Also described is a
CC method for the identification of the animal from a biological sample. The
CC method is used for animal identification to establish the crime with the
CC criminal beyond a reasonable doubt, to establish the identity of
CC biological materials such as skin, horns confiscated from animal
CC poachers, if it is that of an endangered species, for the purpose of
CC molecular evidence of animal hunting and related crime in the court of
CC law, so that human violation of the wildlife resources could be
CC controlled, to have an idea of the geographical location of the
CC commitment of wildlife crime based on the cytochrome b gene haplotype of
CC poached animal identified by the universal primer invented, to detect the
CC adulteration of animal meat in food products for the purpose of food
CC fortification, by the food fortification agencies, to provide a universal
CC technique for detection of the origin of blood or blood stains collected
CC from the scene of the crime related to offenses such as murder and rape,
CC in order to establish the origin of blood found at the scene of the crime
CC when it sounds as if criminals intentionally spread the blood of an
CC animal at the scene of the crime to confuse the crime investigators and
CC forensic scientists with human blood, and so that the method can be
CC converted to a commercial molecular kit and DNA chips based applications
CC for wildlife identification in forensics. The present sequence represents
CC a mitochondrial cytochrome b gene sequence from the present invention

XX
XX
XX Sequence 472 BP; 144 A; 154 C; 62 G; 112 T; 0 U; 0 Other;

Query Match 81.4%; Score 384; DB 8; Length 472;
Best Local Similarity 88.3%; Pred. No. 6.1e-110;
Matches 417; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

Qy 1 TACCATGAGGACAAATATCTTTTGGAGGACAAAGTCATCACCACATCTCTCTTCAGCAA 60
Db 1 TACCATGAGGACAAATATCTTTTGGAGGACAAAGTCATCACCACATCTCTCTTCAGCAA 60


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XX PN WO200277278-A1.
XX PD 03-OCT-2002.
XX PF 28-MAR-2001; 2001WO-IN000055.
XX PR 28-MAR-2001; 2001WO-IN000055.
XX PA (COUL ) COUNCIL SCI & IND RES.
XX PI Verma SK, Singh L;
XX DR WPI; 2003-018945/01.
XX
XX PT New universal primers, mcb 398 and mcb 869, capable of amplifying a
XX PT fragment of cytochrome b gene of any animal species, useful for
XX PT establishing the identity of biological materials and animals for
XX PT molecular evidence in forensics.
XX
XX Example 1; Page 28-57; 128pp; English.
XX
XX The present invention describes universal primers, mcb 398 and mcb 869
XX (see ABQ83297 and ABQ83298), capable of amplifying a fragment of
XX cytochrome b gene of any animal species in polymerase chain reaction
XX (PCR) and revealing the identity of the biological material of any animal
XX of unknown origin at species and sub-species level. Also described is a
XX method for the identification of the animal from a biological sample. The
XX method is used for animal identification to establish the crime with the
XX criminal beyond a reasonable doubt, to establish the identity of
XX biological materials such as skin, horns confiscated from animal
XX poachers, if it is that of an endangered species, for the purpose of
XX molecular evidence of animal hunting and related crime in the court of
XX law, so that human violation of the wildlife resources could be
XX controlled, to have an idea of the geographical location of the
XX commitment of wildlife crime based on the cytochrome b gene haplotype of
XX poached animal identified by the universal primer invented, to detect the
XX adulteration of animal meat in food products for the purpose of food
XX fortification, by the food fortification agencies, to provide a universal
XX technique for detection of the origin of blood or blood stains collected
XX from the scene of the crime related to offenses such as murder and rape,
XX in order to establish the origin of blood found at the scene of the crime,
XX when it sounds as if criminals intentionally spread the blood of an
XX animal at the scene of the crime to confuse the crime investigators and
XX a mitochondrial cytochrome b gene sequence from the present invention
XX
XX Query Match 79.3%; Score 374.4; DB 8; Length 472;
XX Best Local Similarity 87.1%; Pred. No. 6.3e-107;
XX Matches 411; Conservative 0; Mismatches 61; Indels 0; Gaps 0;
XX
XX QY 1 TACCATGAGGACAAATATCTTTTGGAGGAGCAACAGTCATCACCAATCTCCTTTTCAGCAA 60
XX Db 1 TACCATGAGGACAAATATCTTTGAGGAGCTACAGTCATCACTAATCTCTCTCAGCAA 60
XX
XX QY 61 TCCCATACATCGGTACAAACCTAGTAGAATCAATCTCAGGAGGGTTCTCAGTAGATAAG 120
XX Db 61 TCCCATACATCGGACAAACCTAGTCGAATGAATCTGAGGAGGATTTCTCGTAGACAAAG 120
XX
XX QY 121 CAACCCCTTACCGGATTTTTCGCTTCCACTTTATCTCTCCCATTTATCATTCGACCCCTTA 180
XX Db 121 CCACCTTACCGGATTTTTCGCTTTCATTTATCTCTCCCATTTATCATTCGACCCCTCG 180
XX
XX QY 181 CCATAGTACACTACTGTTTCTCCAGGAAACAGGATCCAAACCCACAGGATCTCAT 240
XX Db 181 CTATAGTACATTTTCTCTCTCTCCAGGAAACAGGATCCAAACCCACAGGATTTCCAT 240
XX
XX QY 241 CAGACGAGACAAATTCCTATTCACCCCTACTACATCACTATCAGATATCTAGGAGCTC 300
XX

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Db 241 CAGACACGACAAATCCCATTCACCCCTACTATACAATCAAGACATTCCTAGCGCCA 300
QY 301 TACTATTAAATTTTAAACCTCATGCTTCTAGTCTTATCTCACCAGGACCTGCTTGAGAGC 360
Db 301 TACTATAATCCTTACCCCTTATCTACTAGTATTATTCACACCCGACCTACTTTGGAGAC 360
QY 361 CAGACAACCTATACACCCAGCAACCCACCTTTAATATACACCCCAATATCAAGCCCGAATGAT 420
Db 361 CAGACAACCTATACACCCAGCAACCCACCTTTAATATACACCCCAATATCAAGCCCGAATGAT 420
QY 421 ACTTCCTATTTGCTATACGCAATCTCTCCGATCAATTCCTTAACAACTAGGAGG 472
Db 421 ACTTCCTATTTGCTATACGCAATCTCTCCGATCAATTCCTTAACAACTAGGCGG 472

RESULT 8
ABQ83334
ID ABQ83334 standard; DNA; 472 BP.
XX
XX AC ABQ83334;
XX
XX DT 18-JAN-2003 (first entry)
XX
XX DE Mitochondrial cytochrome b gene sequence SEQ ID NO:39.
XX
XX KW Mitochondrial cytochrome b gene; mitochondrial; cytochrome b;
XX identification; criminal investigation; animal poaching; gene; ds.
XX
XX OS Unidentified.
XX
XX PN WO200277278-A1.
XX
XX PD 03-OCT-2002.
XX
XX PF 28-MAR-2001; 2001WO-IN000055.
XX
XX PR 28-MAR-2001; 2001WO-IN000055.
XX
XX PA (COUL ) COUNCIL SCI & IND RES.
XX
XX PI Verma SK, Singh L;
XX
XX WPI; 2003-018945/01.
XX
XX New universal primers, mcb 398 and mcb 869, capable of amplifying a
XX fragment of cytochrome b gene of any animal species, useful for
XX establishing the identity of biological materials and animals for
XX molecular evidence in forensics.
XX
XX Example 1; Page 28-57; 128pp; English.
XX
XX The present invention describes universal primers, mcb 398 and mcb 869
XX (see ABQ83297 and ABQ83298), capable of amplifying a fragment of
XX cytochrome b gene of any animal species in polymerase chain reaction
XX (PCR) and revealing the identity of the biological material of any animal
XX of unknown origin at species and sub-species level. Also described is a
XX method for the identification of the animal from a biological sample. The
XX method is used for animal identification to establish the crime with the
XX criminal beyond a reasonable doubt, to establish the identity of
XX biological materials such as skin, horns confiscated from animal
XX poachers, if it is that of an endangered species, for the purpose of
XX molecular evidence of animal hunting and related crime in the court of
XX law, so that human violation of the wildlife resources could be
XX controlled, to have an idea of the geographical location of the
XX commitment of wildlife crime based on the cytochrome b gene haplotype of
XX poached animal identified by the universal primer invented, to detect the
XX adulteration of animal meat in food products for the purpose of food
XX fortification, by the food fortification agencies, to provide a universal
XX technique for detection of the origin of blood or blood stains collected
XX from the scene of the crime related to offenses such as murder and rape,
XX in order to establish the origin of blood found at the scene of the crime,
XX when it sounds as if criminals intentionally spread the blood of an
XX animal at the scene of the crime to confuse the crime investigators and
XX a mitochondrial cytochrome b gene sequence from the present invention
XX

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CC forensic scientists with human blood, and so that the method can be
CC converted to a commercial molecular kit and DNA chips based applications
CC for wildlife identification in forensics. The present sequence represents
CC a mitochondrial cytochrome b gene sequence from the present invention
XX
SQ Sequence 472 BP; 141 A; 148 C; 62 G; 121 T; 0 U; 0 Other;

Query Match 79.3%; Score 374.4; DB 8; Length 472;
Best Local Similarity 87.1%; Pred. No. 6.3e-107;
Matches 411; Conservative 0; Mismatches 61; Indels 0; Gaps 0;
QY 1 TACCATGAGGACAAATATCTTTTGGAGGACCAAGTATCAACCAATCTCTTTCAGCAA 60
Db 1 TCCCATGAGGACAAATATCAATCTGAGGAGCCACAGTATTAACCACTCTCTAGCAA 60
QY 61 TCCCATATATCGGTACAAACCTAGTAGAATGAATCTGAGGAGGGTTCCTCAGTAGATAAG 120
Db 61 TCCCATATATCGGCACAAACTTAGTTGAGTGAATCTGAGGGGGCTTTTCAGTAGACAAAG 120
QY 121 CAACCTTACCGATTTTTCGGCTTCCACTTTATCTTCCCATTTATCATTCAGGCCCTTA 180
Db 121 CAACCTTACCGATTTTTCGGCTTCCACTTTATCTTCCCATTTATCATTCAGGCCCTTG 180
QY 181 CCATAGTACACCTACTGTTTCTCCAGAAACAGGATCCAAACCCACAGGAATCTCAT 240
Db 181 CCATAGTCCACCTACTGTTTCTCCAGAAACAGGATCTTAATACCCACAGGAATCTCAT 240
QY 241 CAGAGCAGACAAATATCCATTCACCCCTACTACACTATCAAGATATCTTAGGAGTTC 300
Db 241 CAGAGCAGACAAATATCCGTTTCCACCCCTACTACACTATCAAGATATCTTAGGAGTTC 300
QY 301 TACTATTAATTTTAAACCTCATGCTTCTAGTCTCTATCTCACCGGACCTGCTTGGAGAC 360
Db 301 TATTACTTATCTAGCCCTTAATATCTAGTACTATCTCACCGGACCTTACTCGGAGATC 360
QY 361 CAGACAACTATACACAGCAAAACCCACTTAATACACCCACACATATCAAGCCCGAATGAT 420
Db 361 CAGATTAATATATCTCAGCAAAACCCACTTAACACACTTCCACATCAAGCCCGAATGAT 420
QY 421 ACTTCTTATTTGCATACGCAATCTCCGATCAATCTCTTAACTAGGAGG 472
Db 421 ATTTCCTATTCGGTAGCGCAATCTACGATCAATTCACAAATAAATTAGGAGG 472

RESULT 9
ABQ83303
ID ABQ83303 standard; DNA; 472 BP.
AC ABQ83303;
XX
XX 18-JAN-2003 (first entry)
DE Mitochondrial cytochrome b gene sequence SEQ ID NO:8.
XX
XX Mitochondrial cytochrome b gene; mitochondrial; cytochrome b;
KW identification; criminal investigation; animal poaching; gene; ds.
XX Unidentified.
XX WO200277278-A1.
XX
XX 03-OCT-2002.
XX
XX 28-MAR-2001; 2001WO-IN000055.
XX
XX 28-MAR-2001; 2001WO-IN000055.
XX
XX (COUL) COUNCIL SCI & IND RES.
PA Verma SK, Singh L;
XX WPI; 2003-018945/01.
XX

PT New universal primers, mcb 398 and mcb 869, capable of amplifying a
PT fragment of cytochrome b gene of any animal species, useful for
PT establishing the identity of biological materials and animals for
PT molecular evidence in forensics.

XX Example 1; Page 28-57; 128pp; English.

XX The present invention describes universal primers, mcb 398 and mcb 869
CC (see ABQ83297 and ABQ83298), capable of amplifying a fragment of
CC cytochrome b gene of any animal species in polymerase chain reaction
CC (PCR) and revealing the identity of the biological material of any animal
CC of unknown origin at species and sub-species level. Also described is a
CC method for the identification of the animal from a biological sample. The
CC method is used for animal identification to establish the crime with the
CC criminal beyond a reasonable doubt, to establish the identity of
CC biological materials such as skin, horns confiscated from animal
CC poachers, if it is that of an endangered species, for the purpose of
CC molecular evidence of animal hunting and related crime in the court of
CC law, so that human violation of the wildlife resources could be
CC controlled, to have an idea of the geographical location of the
CC commitment of wildlife crime based on the cytochrome b gene haplotype of
CC poached animal identified by the universal primer invented, to detect the
CC adulteration of animal meat in food products for the purpose of food
CC fortification, by the food fortification agencies, to provide a universal
CC technique for detection of the origin of blood or blood stains collected
CC from the scene of the crime related to offenses such as murder and rape,
CC in order to establish the origin of blood found at the scene of the crime
CC when it sounds as if criminals intentionally spread the blood of an
CC animal at the scene of the crime to confuse the crime investigators and
CC forensic scientists with human blood, and so that the method can be
CC converted to a commercial molecular kit and DNA chips based applications
CC for wildlife identification in forensics. The present sequence represents
CC a mitochondrial cytochrome b gene sequence from the present invention
XX

SQ Sequence 472 BP; 139 A; 152 C; 61 G; 120 T; 0 U; 0 Other;

Query Match 79.0%; Score 372.8; DB 8; Length 472;
Best Local Similarity 86.9%; Pred. No. 2e-106;
Matches 410; Conservative 0; Mismatches 62; Indels 0; Gaps 0;
QY 1 TACCATGAGGACAAATATCTTTTGGAGGACCAAGTATCAACCAATCTCTTTCAGCAA 60
Db 1 TGGCATGAGGACAAATATCATCTGAGGAGCAACAGTATCAACCACTCTCTCAGCAA 60
QY 61 TCCCATATCGGTACAAACCTAGTAGAATGAATCTGAGGAGGGTTCCTCAGTAGATAAG 120
Db 61 TCCCATATATCGGCACAGACCTGGTCAATGAATCTGAGGAGGATCTCGTAGACAAAG 120
QY 121 CAACCTTACCCGATTTTTCGGCTTCCACTTTATCTTCCCATTTATCTGCTGCCCTTG 180
Db 121 CAACCTTACCCGATTTTTCGGCTTCCACTTTATCTTCCCATTTATCTGCTGCCCTTG 180
QY 181 CCATAGTACACCTACTGTTTCTCCAGAAACAGGATCCAAACCCACAGGATCTCAT 240
Db 181 CCATAGTCCATCTACTCTTTTCTCCAGAAACAGGCTCCAAACCCCTACAGGAATCTCT 240
QY 241 CAGACGACGACAAATTCGATTCACCCCTACTACACTATCAAGATATCTTAGGAGCTC 300
Db 241 CAGACACAGACAAATTCGATTCACCCCTACTATACCATTAAGACATCTTAGGCGCCC 300
QY 301 TACTATTAATTTTAAACCTCATGCTTCTAGTCTCTATTTCTCACCGGACCTGCTTGGAGACC 360
Db 301 TACTATTAATTTTAGTCTCTCATACTACTAGTATTTTACACCCGACCTACTTGGAGACC 360
QY 361 CAGACAACTATACACAGCAAAACCCACTTAATACACCCCAATATCAAGCCCGAATGAT 420
Db 361 CAGACAAATATATCCCGAGCAATCCACTTAGCAGCGGCCCTTCACATCAAACTGAATGAT 420
QY 421 ACTTCTTATTTGCATACGCAATCTCCGATCAATCTCTTAACTAGGAGG 472
Db 421 ATTTCTTATTTGCATACGCAATTTCTACGATCAATCCCAACCAACTAGGAGG 472

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RESULT 10
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DT 18-JAN-2003 (first entry)
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DE Mitochondrial cytochrome b gene sequence SEQ ID NO:35.
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XX Mitochondrial cytochrome b gene; mitochondrial; cytochrome b;
KW identification; criminal investigation; animal poaching; gene; ds.
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XX OS Unidentified.
XX
XX PN WO200277278-A1.
XX
XX ED 03-OCT-2002.
XX
XX PF 28-MAR-2001; 2001WO-IN000055.
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XX PR 28-MAR-2001; 2001WO-IN000055.
XX
XX PA (COUL ) COUNCIL SCI & IND RES.
XX
XX PI Verma SK, Singh L;
XX
XX DR WPI; 2003-018945/01.
XX
XX
XX
XX
XX The present invention describes universal primers, mcb 398 and mcb 869
XX (see ABQ83297 and ABQ83298), capable of amplifying a fragment of
XX cytochrome b gene of any animal species in polymerase chain reaction
XX (PCR) and revealing the identity of the biological material of any animal
XX of unknown origin at species and sub-species level. Also described is a
XX method for the identification of the animal from a biological sample. The
XX method is used for animal identification to establish the identity of the
XX criminal beyond a reasonable doubt, to establish the identity of
XX biological materials such as skin, horns confiscated from animal
XX poachers, if it is that of an endangered species, for the purpose of
XX molecular evidence of animal hunting and related crime in the court of
XX law, so that human violation of the wildlife resources could be
XX controlled, to have an idea of the geographical location of the
XX commitment of wildlife crime based on the cytochrome b gene haplotype of
XX poached animal identified by the universal primer invented, to detect the
XX adulteration of animal meat in food products for the purpose of food
XX fortification, by the food fortification agencies, to provide a universal
XX technique for detection of the origin of blood or blood stains collected
XX from the scene of the crime related to offenses such as murder and rape,
XX in order to establish the origin of blood found at the scene of the crime
XX when it sounds as if criminals intentionally spread the blood of an
XX animal at the scene of the crime to confuse the crime investigators and
XX forensic scientists with human blood, and so that the method can be
XX converted to a commercial molecular kit and DNA chips based applications
XX for wildlife identification in forensics. The present sequence represents
XX a mitochondrial cytochrome b gene sequence from the present invention
XX
SQ Sequence 472 BP; 144 A; 163 C; 60 G; 105 T; 0 U; 0 Other;

Query Match 79.0%; Score 372.8; DB 8; Length 472;
Best Local Similarity 86.9%; Pred. No. 2e-106;
Matches 410; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

QY 1 TACCATGAGGACAAATATCTTTTGAGGAGCAACAGTCATCAACAAATCTCTTCAGCAA 60
Db 1 TACCATGAGGACAAATATCTTTTGAGGAGCAACAGTCATCAACAAATCTCTTCAGCAA 60

```

CC biological materials such as skin, horns confiscated from animal
CC poachers, if it is that of an endangered species, for the purpose of
CC molecular evidence of animal hunting and related crime in the court of
CC law, so that human violation of the wildlife resources could be
CC controlled, to have an idea of the geographical location of the
CC commitment of wildlife crime based on the cytochrome b gene haplotype of
CC poached animal identified by the universal primer invented, to detect the
CC adulteration of animal meat in food products for the purpose of food
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CC technique for detection of the origin of blood or blood stains collected
CC from the scene of the crime related to offenses such as murder and rape,
CC in order to establish the origin of blood found at the scene of the crime
CC when it sounds as if criminals intentionally spread the blood of an
CC animal at the scene of the crime to confuse the crime investigators and
CC forensic scientists with human blood, and so that the method can be
CC converted to a commercial molecular kit and DNA chips based applications
CC for wildlife identification in forensics. The present sequence represents
CC a mitochondrial cytochrome b gene sequence from the present invention
XX
SQ Sequence 472 BP; 152 A; 140 C; 57 G; 122 T; 0 U; 1 Other;

Query Match 78.8%; Score 371.8; DB 8; Length 472;
Best Local Similarity 86.7%; Pred. No. 4.1e-106;
Matches 409; Conservative 0; Mismatches 63; Indels 0; Gaps 0;
QY 1 TACCATGAGGACAAATATCTTTTGGAGGACACAGTCTACCATCTCCTTTCAGCAA 60
DB 1 TACCATGAGGACAAATATCTTTTGGAGGACACAGTCTACCATCTCCTTTCAGCAA 60
QY 61 TCCCATACATCGGTACAAACCTAGTAGATGAATCTGAGGAGGTTCTCAGTAGATAAAG 120
DB 61 TCCCATACATCGGTACAAACCTAGTAGATGAATCTGAGGAGGTTCTCAGTAGACAAG 120
QY 121 CAACCCCTTACCCGATTTTTCGCTTTCACCTTTATCTCCCATTTATTCATGAGCAATTG 180
DB 121 CAACCCCTTACCCGATTTTTCGCTTTCACCTTTATCTCCCATTTATTCATGAGCAATTG 180
QY 181 CCATAGTACACCTACTGTTTCTCCAGGACACAGGATCCACACCCACAGGAAATCTCAT 240
DB 181 CCATAGTACACCTACTGTTTCTCCAGGACACAGGATCCACACCCACAGGAAATCTCCT 240
QY 241 CAGACGACAGACAAATTTCCATTCACCCCTACTACACTATCAAGATATCTTAGGAGCTC 300
DB 241 CAGACGACAGACAAATTTCCATTCACCCCTACTACACTATCAAGATATCTTAGGAGCTC 300
QY 301 TACTATTAAATTTTAAACCTCATGCTTCTAGTCTCTATTTCTCACCGGACCTGTTGGAGACC 360
DB 301 TATTACTAATTTCTAATCTAATCTACTAGTACTATTCGACCGGACCTCTCGGAGACC 360
QY 361 CAGACAACTATACACAGGACAAACCCCTTAATACACCCCATATACAGCCCGGAATGAT 420
DB 361 CAGATAACTATACACCCGAGCAAAATCCACTTAACACACCTCCCCACATCAAAACCGAATGAT 420
QY 421 ACTTCTTATTTCATAGCAGCAATCTCCGATCAATTTCTTAACAACTAGGAGG 472
DB 421 ACTTCTTATTTCATANGCAATTTTACGGTCAATCCCCACCAACTAGGAGG 472

RESULT 12
ABQ83313
ID ABQ83313 standard; DNA; 472 BP.
XX
AC ABQ83313;
XX
DT 18-JAN-2003 (first entry)
XX
DE Mitochondrial cytochrome b gene sequence SEQ ID NO:18.
XX
KW Mitochondrial cytochrome b gene; mitochondrial; cytochrome b;
KW identification; criminal investigation; animal poaching; gene; ds.
XX
OS Unidentified.
XX

PN WO200277278-A1.
XX
PD 03-OCT-2002.
XX
PF 28-MAR-2001; 2001WO-IN0000055.
XX
PR 28-MAR-2001; 2001WO-IN0000055.
XX
PA (COUL) COUNCIL SCI & IND RES.
XX
PI Verma SK, Singh L;
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DR WPI; 2003-018945/01.
XX
PT New universal primers, mcb 398 and mcb 869, capable of amplifying a
PT fragment of cytochrome b gene of any animal species, useful for
PT establishing the identity of biological materials and animals for
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XX
PS Example 1; Page 28-57; 128pp; English.
XX
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CC cytochrome b gene of any animal species in polymerase chain reaction
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CC a mitochondrial cytochrome b gene sequence from the present invention
XX
SQ Sequence 472 BP; 147 A; 145 C; 63 G; 117 T; 0 U; 0 Other;
Query Match 78.6%; Score 371.2; DB 8; Length 472;
Best Local Similarity 86.7%; Pred. No. 6.4e-106;
Matches 409; Conservative 0; Mismatches 63; Indels 0; Gaps 0;
QY 1 TACCATGAGGACAAATATCTTTTGGAGGACACAGTCTACCAATCTCCTTTCAGCAA 60
DB 1 TACCATGAGGACAAATATCTTTTGGAGGACACAGTCTATTCACCAATCTATTCAGCAA 60
QY 61 TCCCATACATCGGTACAAACCTAGTAGATGAATCTGAGGAGGTTCTCAGTAGATAAAG 120
DB 61 TCCCATACATCGGTACAAACCTAGTAGATGAATCTGAGGAGGTTCTCAGTAGACAAG 120
QY 121 CAACCCCTTACCCGATTTTTCGCTTTCACCTTTATCTCCCATTTATTCATGAGCCCTTA 180
DB 121 CAACCCCTTACCCGATTTTTCGCTTTCACCTTTATCTCCCATTTATTCATGAGCCCTCG 180
QY 181 CCATAGTACACCTACTGTTTCTCCAGGACAAACAGGATCCACACCCACAGGAAATCTCAT 240
DB 181 CAATATCCATCTACTCTTCTCCATGAAACAGGCTTAACATCCAAACAGGAAATTCAT 240
QY 241 CAGACGACAGACAAATTTCCATTCACCCCTACTACACTATCAAGATATCTTAGGAGCTC 300
DB 241 CAGACGACAGATAAATCCCATTTTCACCCCTACTACACTATTAAGACATTTCTAGGAGCCC 300

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CC animal at the scene of the crime to confuse the crime investigators and
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CC converted to a commercial molecular kit and DNA chips based applications
CC for wildlife identification in forensics. The present sequence represents
CC a mitochondrial cytochrome b gene sequence from the present invention

XX Sequence 472 BP; 143 A; 157 C; 59 G; 113 T; 0 U; 0 Other;

Query Match 78.6%; Score 371.2; DB 8; Length 472;
Best Local Similarity 86.7%; Pred. No. 6.4e-106;
Matches 409; Conservative 0; Mismatches 63; Indels 0; Gaps 0;
QY 1 TACCATTGAGGACAAATATCTTTTGGAGGACCAACAGTCATCACCAATCTCTTTTCAGCAA 60
DB 1 TACCATTGAGGACAAATATCTTTGAGGACCAACAGTCATCACCAATCTCTTTTCAGCAA 60
QY 61 TCCCATACATCGGTACAACTAGTAGAATCTGAGGAGGTTCTCAGTAGATAAG 120
DB 61 TTCCATATATTGGCAACAACTAGTGAATGAATCTGAGGGGATCTCAGTAGACAAAG 120
QY 121 CAACCCCTTACCCGATTTTTCGCTTCCACTTTATCTCTCCATTTATCATTCGAGCCCTTA 180
DB 121 CCACCCCTGACCCGATTTTTCGCTTTCACCTTTATTTCCCATTCATCTCGAGCCCTCG 180
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DB 241 CGGACACAGATAAATTCCTTCCACCCCTTACTACACCATTAAGACATCTAGTGCCA 300
QY 301 TACTATTAAATTTAAACCTCATGCTTCTAGTCCCTATTCTACCCGACCTGCTTGGAGACC 360
DB 301 TCCTACTAATCTCACTCATCTACTAGTACTATTACGCGCTGACTACTCGAGACC 360
QY 361 CAGACAACTATACACGAGAAACCCATTATATACACCCCAATATCAAGCCCAATGAT 420
DB 361 CAGACAACTATACACCCGAGAAACCCATTATATACACCCCTTCAATCAAACTGAATGAT 420
QY 421 ACTTCTTATTGCTAGCATCTCTCGATCAATTTCTTACACTAGGAGG 472
DB 421 ACTTCTTATTGCTAGCATCTTACGATCAATTTCTTACACTAGGAGG 472

RESULT 15

ABQ83310
ID ABQ83310 standard; DNA; 472 BP.

XX AC ABQ83310;

XX DT 18-JAN-2003 (first entry)

XX DE Mitochondrial cytochrome b gene sequence SEQ ID NO:15.

XX KW Mitochondrial cytochrome b gene; mitochondrial; cytochrome b;
XX identification; criminal investigation; animal poaching; gene; ds.

XX OS Unidentified.

XX PN WO200277278-A1.

XX PD 03-OCT-2002.

XX PF 28-MAR-2001; 2001WO-IN000055.

XX PR 28-MAR-2001; 2001WO-IN000055.

XX PA (COUL) COUNCIL SCI & IND RES.

XX PI Verma SK, Singh L;

XX DR WPI; 2003-018945/01.

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CC controlled, to have an idea of the geographical location of the
CC commitment of wildlife crime based on the cytochrome b gene haplotype of
CC poached animal identified by the universal primer invented, to detect the
CC adulteration of animal meat in food products for the purpose of food
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CC from the scene of the crime related to offenses such as murder and rape,
CC in order to establish the origin of blood found at the scene of the crime
CC when it sounds as if criminals intentionally spread the blood of an
CC animal at the scene of the crime to confuse the crime investigators and
CC forensic scientists with human blood, and so that the method can be
CC converted to a commercial molecular kit and DNA chips based applications
CC for wildlife identification in forensics. The present sequence represents
CC a mitochondrial cytochrome b gene sequence from the present invention

XX Sequence 472 BP; 139 A; 157 C; 61 G; 115 T; 0 U; 0 Other;

Query Match 78.3%; Score 369.6; DB 8; Length 472;
Best Local Similarity 86.4%; Pred. No. 2e-105;
Matches 408; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 1 TACCATTGAGGACAAATATCTTTTGGAGGACCAACAGTCATCACCAATCTCTTTTCAGCAA 60

DB 1 TACCATTGAGGACAAATATCTTTTGGAGGACCAACAGTCATCACCAATCTCTTTTCAGCAA 60

QY 61 TCCCATACATCGGTACAAACCTAGTAGAATCTGAGGAGGTTCTCAGTAGATAAG 120


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SOURCE      mitochondrion Perissocephalus tricolor (capuchinbird)
ORGANISM    Perissocephalus tricolor
REFERENCE    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS     Archosauaria; Aves; Neognathae; Passeriformes; Cotingidae;
TITLE       Perissocephalus.
JOURNAL     1 (bases 1 to 327)
REFERENCE    Prum,R.O., Rice,N.H., Mobley,J.A. and Dimmick,W.W.
AUTHORS     A Preliminary Phylogenetic Hypothesis for the Cotingas (Cotingidae)
TITLE       Based on Mitochondrial DNA
JOURNAL     Auk 117 (1), 236-241 (2000)
REFERENCE    2 (bases 1 to 327)
AUTHORS     Prum,R.O., Rice,N.H., Mobley,J.A. and Dimmick,W.W.
TITLE       Direct Submission
JOURNAL     Submitted (26-JAN-1999) Systematics and Ecology, University of
            Kansas, Natural History Museum, Lawrence, KS 66045, USA
FEATURES    Location/Qualifiers
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            /db_xref="GI:8050380"
            /translation="WYFLFAVAILRSIPKPGVLAASVLLIIPFLHMSKQRTM
            AFRPLSQFLWLVANLLILTWIGSQPVEHPFIIGQLASVAYFTLLILPFIIGALE
            NKILNL"
ORIGIN
Query Match      100.0%; Score 26; DB 5; Length 327;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTCTAGTTTGTAGGATTGATCG 26
    |||
Db 56 CCTCTAGTTTGTAGGATTGATCG 31
    |||

RESULT 3
AF123617/c
LOCUS      AF123617      375 bp      DNA      linear      VRT 01-MAY-2002
DEFINITION Pipreola arcuata cytochrome b gene, partial cds; mitochondrial gene
            for mitochondrial product.
ACCESSION  AF123617
VERSION     AF123617.1 GI:8050348
KEYWORDS
SOURCE      .
ORGANISM    mitochondrion Pipreola arcuata (barred fruiteater)
            Pipreola arcuata
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Archosauaria; Aves; Neognathae; Passeriformes; Cotingidae; Pipreola.
REFERENCE    1 (bases 1 to 375)
AUTHORS     Prum,R.O., Rice,N.H., Mobley,J.A. and Dimmick,W.W.
TITLE       A Preliminary Phylogenetic Hypothesis for the Cotingas (Cotingidae)
            Based on Mitochondrial DNA
JOURNAL     Auk 117 (1), 236-241 (2000)
REFERENCE    2 (bases 1 to 375)
AUTHORS     Prum,R.O., Rice,N.H., Mobley,J.A. and Dimmick,W.W.
TITLE       Direct Submission
JOURNAL     Submitted (26-JAN-1999) Systematics and Ecology, University of
            Kansas, Natural History Museum, Lawrence, KS 66045, USA
FEATURES    Location/Qualifiers
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            /db_xref="GI:8050348"
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CDS
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            /organelle="mitochondrion"
            /mol_type="genomic DNA"
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            /codon_start=1
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            /db_xref="GI:8050348"
            /translation="WYFLFAVAILRSIPKPGVLAASVLLIIPFLHMSKQRTM
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            NKILNL"

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SOURCE      mitochondrion Perissocephalus tricolor (capuchinbird)
ORGANISM    Perissocephalus tricolor
REFERENCE    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS     Archosauaria; Aves; Neognathae; Passeriformes; Cotingidae;
TITLE       Perissocephalus.
JOURNAL     1 (bases 1 to 327)
REFERENCE    Prum,R.O., Rice,N.H., Mobley,J.A. and Dimmick,W.W.
AUTHORS     A Preliminary Phylogenetic Hypothesis for the Cotingas (Cotingidae)
TITLE       Based on Mitochondrial DNA
JOURNAL     Auk 117 (1), 236-241 (2000)
REFERENCE    2 (bases 1 to 327)
AUTHORS     Prum,R.O., Rice,N.H., Mobley,J.A. and Dimmick,W.W.
TITLE       Direct Submission
JOURNAL     Submitted (26-JAN-1999) Systematics and Ecology, University of
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FEATURES    Location/Qualifiers
            source
            1..327
            /organism="Perissocephalus tricolor"
            /organelle="mitochondrion"
            /mol_type="genomic DNA"
            /db_xref="taxon:114366"
            <1..327
            /codon_start=1
            /transl_table=2
            /product="cytochrome b"
            /protein_id="AAF71639.1"
            /db_xref="GI:8050380"
            /translation="WYFLFAVAILRSIPKPGVLAASVLLIIPFLHMSKQRTM
            AFRPLSQFLWLVANLLILTWIGSQPVEHPFIIGQLASVAYFTLLILPFIIGALE
            NKILNL"
ORIGIN
Query Match      100.0%; Score 26; DB 5; Length 327;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTCTAGTTTGTAGGATTGATCG 26
    |||
Db 104 CCTCTAGTTTGTAGGATTGATCG 79
    |||

RESULT 4
AF127194/c
LOCUS      AF127194      378 bp      DNA      linear      VRT 08-MAY-2000
DEFINITION Grallaria guatimalensis cytochrome b gene, partial cds;
            mitochondrial gene for mitochondrial product.
ACCESSION  AF127194
VERSION     AF127194.1 GI:7715712
KEYWORDS
SOURCE      .
ORGANISM    mitochondrion Grallaria guatimalensis (scaled antpitta)
            Grallaria guatimalensis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Archosauaria; Aves; Neognathae; Passeriformes; Formicariidae;
            Grallaria.
REFERENCE    1 (bases 1 to 378)
AUTHORS     Krabbe,N., Agro,D.J., Rice,N.H., Jacome,M., Navarrete,L. and
            Sornoza,M.F.
TITLE       A new species of antpitta (Formicariidae: Grallaria) from the
            southern Ecuadorian Andes
JOURNAL     Auk 116 (4), 882-890 (1999)
REFERENCE    2 (bases 1 to 378)
AUTHORS     Krabbe,N., Agro,D.J., Rice,N.H., Jacome,M., Navarrete,L. and
            Sornoza,M.F.
TITLE       Direct Submission
JOURNAL     Submitted (10-FEB-1999) Ecology and Evolutionary Biology,
            University of Kansas, Natural History Museum, Lawrence, KS 66045,
            USA
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Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTCTAGTTTGTAGGATTGATCG 26
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Db 107 CCTCTAGTTTGTAGGATTGATCG 82
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RESULT 5
AF127202/c
LOCUS      AF127202      378 bp      DNA      linear      VRT 08-MAY-2000
DEFINITION Hylopezus fulviventris cytochrome b gene, partial cds;

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mitochondrial gene for mitochondrial product.

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ACCESSION   AF127202
VERSION     AF127202.1  GI:7715727
KEYWORDS
SOURCE      mitochondrial Hylopezus fulviventris (fulvous-bellied antpitta)
ORGANISM    Hylopezus fulviventris
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Archosauria; Aves; Neognathae; Passeriformes; Formicariidae;
            Hylopezus.
REFERENCE   1 (bases 1 to 378)
AUTHORS     Krabbe,N., Agro,D.J., Rice,N.H., Jacome,M., Navarrete,L. and
            Sornoz,M.F.
TITLE       A new species of antpitta (Formicariidae: Grallaria) from the
            southern Ecuadorian Andes
JOURNAL     Auk 116 (4):882-890 (1999)
REFERENCE   2 (bases 1 to 378)
AUTHORS     Krabbe,N., Agro,D.J., Rice,N.H., Jacome,M., Navarrete,L. and
            Sornoz,M.F.
TITLE       Direct Submission
JOURNAL     Submitted (10-FEB-1999) Ecology and Evolutionary Biology,
            University of Kansas, Natural History Museum, Lawrence, KS 66045,
            USA
FEATURES
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Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 107 CCTCCTAGTTTGTAGGATTGATCG 82
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RESULT 6
LOCUS      AX565570/c
DEFINITION Sequence 11 from Patent WO02077278.
ACCESSION  AX565570
VERSION    AX565570.1  GI:26000920
KEYWORDS
SOURCE     Alcelaphus buselaphus (hartebeest)
ORGANISM   Alcelaphus buselaphus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
            Alcelaphinae; Alcelaphus.
REFERENCE   1
AUTHORS     Verma,S.K. and Singh,L.
TITLE       Universal primers for wildlife identification
JOURNAL     Patent: WO 02077278-A 11 03-OCT-2002;
            Council of Scientific and Industrial Research (IN)
            Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 107 CCTCCTAGTTTGTAGGATTGATCG 82
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RESULT 6
LOCUS      AX565570/c
DEFINITION Sequence 11 from Patent WO02077278.
ACCESSION  AX565570
VERSION    AX565570.1  GI:26000920
KEYWORDS
SOURCE     Alcelaphus buselaphus (hartebeest)
ORGANISM   Alcelaphus buselaphus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
            Alcelaphinae; Alcelaphus.
REFERENCE   1
AUTHORS     Verma,S.K. and Singh,L.
TITLE       Universal primers for wildlife identification
JOURNAL     Patent: WO 02077278-A 11 03-OCT-2002;
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Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 107 CCTCCTAGTTTGTAGGATTGATCG 82
    |||

mitochondrial gene for mitochondrial product.
Query Match      100.0%; Score 26; DB 6; Length 472;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 472 CCTCCTAGTTTGTAGGATTGATCG 447
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RESULT 7
LOCUS      AX565571/c
DEFINITION Sequence 12 from Patent WO02077278.
ACCESSION  AX565571
VERSION    AX565571.1  GI:26000921
KEYWORDS
SOURCE     Sigmoceros lichtensteini (Lichtenstein's hartebeest)
ORGANISM   Sigmoceros lichtensteini
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
            Alcelaphinae; Sigmoceros.
REFERENCE   1
AUTHORS     Verma,S.K. and Singh,L.
TITLE       Universal primers for wildlife identification
JOURNAL     Patent: WO 02077278-A 12 03-OCT-2002;
            Council of Scientific and Industrial Research (IN)
            Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 472 CCTCCTAGTTTGTAGGATTGATCG 447
    |||

RESULT 8
LOCUS      AF376882/c
DEFINITION Yuhina zantholeuca cytochrome b gene, partial cds; mitochondrial
            gene for mitochondrial product.
ACCESSION  AF376882
VERSION    AF376882.1  GI:21309969
KEYWORDS
SOURCE     mitochondrion Yuhina zantholeuca
ORGANISM   Yuhina zantholeuca
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Archosauria; Aves; Neognathae; Passeriformes; Corvoidea; Corvidae;
            Yuhina.
REFERENCE   1 (bases 1 to 477)
AUTHORS     Cibois,A., Kalyakin,M.V., Han,L.-X. and Pasquet,E.
TITLE       Molecular phylogenetics of babblers (Timaliidae): reevaluation of
            the genera Yuhina and Stachyris
JOURNAL     J. Avian Biol. 33 (4), 380-390 (2002)
REFERENCE   2 (bases 1 to 477)
AUTHORS     Cibois,A., Kalyakin,M., Han,L.-X. and Pasquet,E.
TITLE       Direct Submission
JOURNAL     Submitted (07-MAY-2001) Ornithology, Museum National d'Histoire
            Naturelle, 55 rue Buffon, Paris 75005, France
REFERENCE   3 (bases 1 to 477)
AUTHORS     Cibois,A., Kalyakin,M., Han,L.-X. and Pasquet,E.
TITLE       Direct Submission
JOURNAL     Submitted (20-JUN-2002) Ornithology, Museum National d'Histoire
            Naturelle, 55 rue Buffon, Paris 75005, France
REMARK     Sequence update by submitter
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            Location/Qualifiers
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ORIGIN
Query Match 100.0%; Score 26; DB 5; Length 477;
Best Local Similarity 100.0%; Pred. No. 1.2; Mismatches 0; Indels 0; Gaps 0;
Matches 26; Conservative 0;

Qy 1 CCTCTAGTTTGTAGGATTGATCG 26
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Db 353 CCTCTAGTTTGTAGGATTGATCG 328
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RESULT 9
CFU81343/c
LOCUS
DEFINITION Chelus fimbriata cytochrome b gene, mitochondrial gene encoding
mitochondrial protein, partial cds.
ACCESSION U81343
VERSION U81343.1 GI:2098650
KEYWORDS
SOURCE
ORGANISM
mitochondrion Chelus fimbriatus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Testudines; Pleurodira; Chelidae; Chelus.
REFERENCE
1 (bases 1 to 892)
Shaffer, H.B., Meylan, P. and McKnight, M.L.
TITLE Tests of turtle phylogeny: molecular, morphological, and
paleontological approaches
JOURNAL Syst. Biol. 46 (2), 235-268 (1997)
MEDLINE 21971902
PUBMED 11975342
REFERENCE
2 (bases 1 to 892)
Shaffer, H.B., Meylan, P. and McKnight, M.L.
DIRECT SUBMISSION
AUTHORS
TITLE
JOURNAL
SUBMITTED (09-DEC-1996) Evolution & Ecology, University of
California, Davis, CA 95616, USA
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Location/Qualifiers
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ORIGIN
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Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 791 CCTCTAGTTTGTAGGATTGATCG 766
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RESULT 10
AY150649/c
LOCUS
DEFINITION Andronon aequatorialis cytochrome b gene, partial cds;
mitochondrial gene for mitochondrial product.
ACCESSION AY150649
VERSION AY150649.1 GI:37195387
KEYWORDS
SOURCE
ORGANISM
mitochondrion Andronon aequatorialis (tooth-billed hummingbird)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Trochiliformes; Trochilidae;
Andronon.
1 (bases 1 to 912)
Bleiwiss, R., Hendrickson, S.L., Berres, M.E., Willis, Y.O. and
Willis, E.O.
TITLE Affinities of the saw-billed hermit (Ramphodon naevius) determined
by cytochrome-b sequence data
JOURNAL Wilson Bull. (2003) In press
REFERENCE
2 (bases 1 to 912)
Bleiwiss, R., Hendrickson, S.L., Berres, M.E., Willis, Y.O. and
Willis, E.O.
DIRECT SUBMISSION
TITLE
JOURNAL
SUBMITTED (16-SEP-2002) Department of Zoology and the Zoological
Museum, University of Wisconsin, 250 North Mills Street, Madison,
WI 53706, USA
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RESULT 11
U86834/c
LOCUS
DEFINITION Phyllotis wolffsohni MSB 67270 cytochrome b (cytb) gene,
mitochondrial gene encoding mitochondrial protein, partial cds.
ACCESSION U86834
VERSION U86834.1 GI:4218914
KEYWORDS
SOURCE
ORGANISM
mitochondrion Phyllotis wolffsohni (Wolffsohn's leaf-eared mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
Phyllotis.
1 (bases 1 to 929)
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AUTHORS Steppan, S.J.
 TITLE Phylogenetic relationships and species limits within Phyllostis (Rodentia: Sigmodontinae): concordance between mtDNA sequence and morphology
 JOURNAL J. Mammal., 79 (2), 573-593 (1998)
 REFERENCE 2 (bases 1 to 929)
 AUTHORS Steppan, S.J.
 TITLE Direct Submission
 JOURNAL Submitted (24-JAN-1997) Laboratory of Molecular Systematics, Smithsonian Institution, Museum Support Center, 4210 Silver Hill Road, Suitland, MD 20746, USA
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 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 LOCUS Lochnias nematura cytochrome b (cytb) gene, partial cds;
 DEFINITION mitochondrial gene for mitochondrial product.
 ACCESSION AY065699
 VERSION 1
 KEYWORDS
 SOURCE AY065699.1 GI:21805434
 ORGANISM Lochnias nematura
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Passeriformes; Furnariidae; Lochnias.
 REFERENCE 1 (bases 1 to 999)
 AUTHORS Irestedt, M., Fjeldsa, J., Johansson, U.S. and Ericson, P.G.P.
 TITLE Systematic relationships and biogeography of the tracheophone subscines (Aves: Passeriformes)
 JOURNAL Mol. Phylogenet. Evol. 23 (3), 499-512 (2002)
 MEDLINE PUBMED 1209801
 REFERENCE 2 (bases 1 to 999)
 AUTHORS Irestedt, M., Fjeldsa, J., Johansson, U.S. and Ericson, P.G.P.
 TITLE Direct Submission
 JOURNAL Submitted (05-DEC-2001) Dept. of Vertebrate Zoology, Swedish Museum of Natural History, P.O. Box 50007, Stockholm SE-10405, Sweden
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 Best Local Similarity 100.0%; Pred. No. 0.93;
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 Db 728 CCTCTAGTTTCTTAGGATTCATCG 703
 RESULT 13
 AY065721/c
 LOCUS Hylopezus fulviventris cytochrome b (cytb) gene, partial cds;
 DEFINITION mitochondrial gene for mitochondrial product.
 ACCESSION AY065721
 VERSION 1
 KEYWORDS
 SOURCE AY065721.1 GI:21805478
 ORGANISM Hylopezus fulviventris
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Passeriformes; Formicariidae; Hylopezus.
 REFERENCE 1 (bases 1 to 999)
 AUTHORS Irestedt, M., Fjeldsa, J., Johansson, U.S. and Ericson, P.G.P.
 TITLE Systematic relationships and biogeography of the tracheophone subscines (Aves: Passeriformes)
 JOURNAL Mol. Phylogenet. Evol. 23 (3), 499-512 (2002)
 MEDLINE PUBMED 1209801
 REFERENCE 2 (bases 1 to 999)
 AUTHORS Irestedt, M., Fjeldsa, J., Johansson, U.S. and Ericson, P.G.P.
 TITLE Direct Submission
 JOURNAL Submitted (05-DEC-2001) Dept. of Vertebrate Zoology, Swedish Museum of Natural History, P.O. Box 50007, Stockholm SE-10405, Sweden
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ORIGIN

Query Match 100.0%; Score 26; DB 5; Length 999;
Best Local Similarity 100.0%; Pred. No. 0.93;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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|||||
Db 728 CCTCCTAGTTTGTAGGATTGATCG 703

RESULT 14
AF189111/c
LOCUS
DEFINITION Cryptotermes austrinus cytochrome b (Cytb) gene, partial cds; mitochondrial gene for mitochondrial product.
ACCESSION AF189111
VERSION AF189111.1 GI:10441542
KEYWORDS
SOURCE mitochondrion Cryptotermes austrinus

ORGANISM
Cryptotermes austrinus
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Orthopteroidea; Dictyoptera; Isoptera; Kalotermitidae;
Cryptotermitinae; Cryptotermes.

REFERENCE
AUTHORS Thompson, G.J., Miller, J.R., Lenz, M. and Crozier, R.H.
TITLE Phylogenetic analysis and trait evolution in Australian lineages of drywood termites (Isoptera, Kalotermitidae)
JOURNAL Mol. Phylogenet. Evol. 17 (3), 419-429 (2000)

MEDLINE
20575775
PUBMED 11131196

REFERENCE
AUTHORS Thompson, G.J. and Crozier, R.H.
TITLE Direct Submission
JOURNAL Submitted (22-SEP-1999) Genetics & Evolution, La Trobe University, Kingsbury Drive, Melbourne, VIC 3083, Australia
FEATURES
Location/Qualifiers

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/db_xref="GI:10441543"

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SLKEPYLLGDPDFINPLNPLVPHIQPEWYFLFAYAILRSIKLGGVIALAWSTAI
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Query Match 100.0%; Score 26; DB 3; Length 1056;
Best Local Similarity 100.0%; Pred. No. 0.92;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTCCTAGTTTGTAGGATTGATCG 26
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Db 797 CCTCCTAGTTTGTAGGATTGATCG 772

RESULT 15

AY188015/c

LOCUS
DEFINITION

ACCESSION
VERSION
KEYWORDS
SOURCE

ORGANISM
mitochondrion Dromicodryas quadrilineatus

REFERENCE
AUTHORS
TITLE

JOURNAL
REFERENCE
AUTHORS

TITLE
JOURNAL

REFERENCE
AUTHORS
TITLE

JOURNAL
REFERENCE
AUTHORS

TITLE
JOURNAL

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TITLE

JOURNAL
REFERENCE
AUTHORS

TITLE
JOURNAL

REMARK
FEATURES

Location/Qualifiers
source

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/mol_type="genomic DNA"
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/db_xref="GI:37778273"

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SINDPTTRFFAIFHILFPAILLSLSIIHLLHNEGSSNPGLNSDIDKIPFPYHSY
KDTLMTLITMLLVMSFTPNFNDPENFSKANPLVTPQHKPEWYFLPAYGILRSI
PNKLGSTLALLMSVTILISMPFTHTSNIRTMTPRMAQLMFWTLATFITITWAATKP
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ORIGIN

Query Match 100.0%; Score 26; DB 5; Length 1111;
Best Local Similarity 100.0%; Pred. No. 0.9;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTCCTAGTTTGTAGGATTGATCG 26
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Db 845 CCTCCTAGTTTGTAGGATTGATCG 820

Search completed: November 17, 2004, 02:58:40
Job time : 145.229 secs

AY188015
Dromicodryas quadrilineatus cytochrome b (cyt b) gene, complete cds; mitochondrial gene for mitochondrial product.

AY188015
AY188015.1 GI:37778272

mitochondrion Dromicodryas quadrilineatus
Dromicodryas quadrilineatus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Colubridae; Boodontinae; Dromicodryas.

1 (bases 1 to 1111)
Nagy, Z.T., Joger, U., Wink, M., Glaw, F. and Vences, M.
Multiple colonization of Madagascar and Socotra by colubrid snakes:
evidence from nuclear and mitochondrial gene phylogenies
Proc. R. Soc. Lond., B, Biol. Sci. 270, 2613-2621 (2003)

2 (bases 1 to 1111)
Nagy, Z.T., Joger, U., Wink, M., Glaw, F. and Vences, M.
Direct Submission
Submitted (25-NOV-2002) Department of Pharmacy and Molecular
Biotechnology, Biological Section, University of Heidelberg, Im
Neuenheimer Feld 364, Heidelberg 69120, Germany

3 (bases 1 to 1111)
Nagy, Z.T., Joger, U., Wink, M., Glaw, F. and Vences, M.
Direct Submission
Submitted (27-OCT-2003) Department of Pharmacy and Molecular
Biotechnology, Biological Section, University of Heidelberg, Im
Neuenheimer Feld 364, Heidelberg 69120, Germany

Sequence update by submitter
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/organelle="mitochondrion"
/mol_type="genomic DNA"
/db_xref="taxon:224545"

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/notes="TAA stop codon is completed by the addition of 3' A residues to the mRNA"

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/transl_table=2
/product="cytochrome b"

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/translations="MSNQHMLTFLNLLPVGINISSWVNFSGTLLACLMLQTTGFFLA
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EWLSCGTLITLMTATAFGYVLPWQMSFWAATVITNLLTAIPYIGTILTWLWGGF
SINDPTTRFFAIFHILFPAILLSLSIIHLLHNEGSSNPGLNSDIDKIPFPYHSY
KDTLMTLITMLLVMSFTPNFNDPENFSKANPLVTPQHKPEWYFLPAYGILRSI
PNKLGSTLALLMSVTILISMPFTHTSNIRTMTPRMAQLMFWTLATFITITWAATKP
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Result No.	Score	Query Match	Length	DB	ID	Description	
1	286.4	60.7	16568	4	US-09-525-906-1	Sequence 1, Appli	
2	286.4	60.7	16569	3	US-09-097-889-2	Sequence 2, Appli	
3	286.4	60.7	16569	3	US-09-377-856-1	Sequence 1, Appli	
4	286.4	60.7	16569	4	US-09-302-681-2	Sequence 2, Appli	
5	286.4	60.7	16569	4	US-09-098-079-2	Sequence 2, Appli	
6	286.4	60.7	16569	4	US-10-053-611-1	Sequence 1, Appli	
7	284.8	60.3	11440	4	US-09-377-497-7	Sequence 7, Appli	
8	195	41.3	614	3	US-09-385-982-185	Sequence 185, App	
c 9	182	38.6	591	3	US-09-385-982-493	Sequence 493, App	
c 10	179.6	38.1	602	3	US-09-385-982-375	Sequence 375, App	
c 11	149.4	31.7	619	3	US-09-385-982-510	Sequence 510, App	
c 12	146	30.9	578	3	US-09-328-111-763	Sequence 763, App	
c 13	130.4	27.6	597	3	US-09-328-111-562	Sequence 562, App	
c 14	127.8	27.1	650	3	US-08-998-416-190	Sequence 190, App	
c 15	127.8	27.1	716	3	US-08-998-416-1032	Sequence 1032, App	
c 16	127.8	27.1	835	3	US-08-998-416-533	Sequence 533, App	
c 17	127.8	27.1	836	3	US-08-998-416-286	Sequence 286, App	
c 18	126.4	26.8	668	3	US-09-328-111-812	Sequence 812, App	
19	101.4	21.5	255	4	US-09-702-705-719	Sequence 719, App	
20	101.4	21.5	255	4	US-09-736-457-719	Sequence 719, App	
21	101.4	21.5	255	4	US-09-614-124B-719	Sequence 719, App	
22	101.4	21.5	255	4	US-09-671-325-719	Sequence 719, App	
23	101.4	21.5	255	4	US-09-589-184-719	Sequence 719, App	
24	101.4	21.5	255	4	US-09-658-824-719	Sequence 719, App	
25	82.6	17.5	321	4	US-09-348-796A-1425	Sequence 1425, App	
26	79.4	16.8	315	4	US-09-313-294A-7516	Sequence 7516, App	
27	64.6	13.7	759	4	US-09-370-767-11513	Sequence 11513, App	

Db 15504 CAGACAAATATACCTAGCCACACCTTAAACACCTCCACATCAAGCCGGAATGAT 15563
QY 421 ACTTCTATTGTCATACGCAATCTCCGATCAATCTTAAACAACTAGGAGG 472
Db 15564 ATTTCCTATTGCTTACACAAATCTCCGATCGTCCCTAACAACTAGGAGG 15615

RESULT 4
US-09-302-681-2
; Sequence 2, Application US/09302681
; Patent No. 6441149
; GENERAL INFORMATION:
; APPLICANT: Hermsstadt, Corrina
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Clevenger, William
; APPLICANT: Fahy, Eoin F.
; APPLICANT: Davis, Robert E.
; TITLE OF INVENTION: DIAGNOSTIC METHOD OF EXTRAMITOCHONDRIAL DNA
; FILE REFERENCE: 660088.416C1
; CURRENT APPLICATION NUMBER: US/09/302,681
; CURRENT FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2: 16569
; LENGTH: 16569
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-302-681-2

Query Match 60.7%; Score 286.4; DB 4; Length 16569;
Best Local Similarity 75.4%; Pred. No. 5.3e-86;
Matches 356; Conservative 0; Mismatches 116; Indels 0; Gaps 0;
QY 1 TACCATGAGGACAAATATCTTTTGGAGGACAACTAGTCAATCTCTTTCAGCAA 60
Db 15144 TCCCGTGAGGCCAAATATCATCTGAGGGGCCACAGTAATACAACTTACTATCGCCA 15203

QY 61 TCCCATACATCGGTACAAACCTAGTAGAATGAATCTGAGGAGGGTCTCAGTAGATAAG 120
Db 15204 TCCCATACATTTGGGACAGACCTAGTTCAATGAATCTGAGGAGGCTACTCAGTAGACAGTC 15263
QY 121 CAACCTTACCCGATTTTGGCTTCCACCTTATCTCCCATTTATCATTTGAGGAGCCCTTA 180
Db 15264 CCACCTTCACAGATTTCTTACCTTTACCTTCACTTCTGAGGAGGCTACTCAGTAGACAGTC 15323

QY 181 CCATAGTACACCTACTGTTTCTCCAGAAACAGGATCCAAACCCACAGGAATCTCAT 240
Db 15324 CAACCTTCCACCTCTTATTTGCAAGAACGGGATCAACACCCCTAGGATCACCT 15383
QY 241 CAGACGACAGCAAAATTCACCTTCCACCTTACTACACTATCAAAGATATCCTAGGAGTC 300
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QY 421 ACTTCTATTGTCATAGCAATCTCCGATCAATTTCTTAAACAACTAGGAGG 472
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RESULT 5
US-09-098-079-2
; Sequence 2, Application US/09098079
; Patent No. 6489095
; GENERAL INFORMATION:

; APPLICANT: Hermsstadt, Corrina
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Clevenger, William
; APPLICANT: Fahy, Eoin F.
; APPLICANT: Davis, Robert E.
; TITLE OF INVENTION: DIAGNOSTIC METHOD BASED ON QUANTIFICATION OF
; TITLE OF INVENTION: EXTRAMITOCHONDRIAL DNA
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/098,079
; FILING DATE: 15-JUN-1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Rosenman Ph.D., Stephen J.
; REGISTRATION NUMBER: 43,058
; REFERENCE/DOCKET NUMBER: 660088.416
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16569 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-098-079-2

Query Match 60.7%; Score 286.4; DB 4; Length 16569;
Best Local Similarity 75.4%; Pred. No. 5.3e-86;
Matches 356; Conservative 0; Mismatches 116; Indels 0; Gaps 0;
QY 1 TACCATGAGGACAAATATCTTTTGGAGGACAACTAGTCAATCTCTTTCAGCAA 60
Db 15144 TCCCGTGAGGCCAAATATCATCTGAGGGGCCACAGTAATACAACTTACTATCGCCA 15203
QY 61 TCCCATACATCGGTACAAACCTAGTAGAATGAATCTGAGGAGGGTCTCAGTAGATAAG 120
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QY 121 CAACCTTACCCGATTTTGGCTTCCACCTTATCTCCCATTTATCATTTGAGGAGCCCTTA 180
Db 15264 CCACCTTCACAGATTTCTTACCTTTACCTTCACTTCTGAGGAGGCTACTCAGTAGACAGTC 15323
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Db 15324 CAACCTTCCACCTCTTATTTGCAAGAACGGGATCAACACCCCTAGGATCACCT 15383
QY 241 CAGACGACAGCAAAATTCACCTTCCACCTTACTACACTATCAAAGATATCCTAGGAGTC 300
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QY 301 TACTATTAAATTTAAACCTCATGCTTCTAGTCTTATCTCAGCGGACCTCTTGGAGACC 360
Db 15444 TTCTCTTCTCTCTCTCTTAATGACATTAACATTTCTCACCAGACCTCTTAGGAGACC 15503
QY 361 CAGACAACTATACACGACAAACCCACTTAATACACCCCCACATATCAAAGCCGGAATGAT 420
Db 15504 CAGACAAATTAACCTTAGCCAAACCCCTTAAACACCCCTCCACATCAAGCCGGAATGAT 15563
QY 421 ACTTCTATTGTCATAGCAATCTCCGATCAATTTCTTAAACAACTAGGAGG 472

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Db      15564  ATTTCCTATTGCGCTACACAATTTCGATCCGTCCTCCCTAACAACTAGGAGG  15615

RESULT 6
US-10-053-611-1
; Sequence 1, Application US/10053611
; Patent No. 6750021
; GENERAL INFORMATION:
; APPLICANT: Polyak, Kornelia
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; TITLE OF INVENTION: Subtle Mitochondrial Mutations as Tumor
; TITLE OF INVENTION: Markers
; FILE REFERENCE: 1107.82346
; CURRENT APPLICATION NUMBER: US/10/053,611
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: US/09/377,856
; PRIOR FILING DATE: 1999-08-20
; PRIOR APPLICATION NUMBER: 60/097,307
; PRIOR FILING DATE: 1998-08-20
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 16569
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-053-611-1

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Query Match	60.7%	Score 286.4	DB 4	Length 16569
Best Local Similarity	75.4%	Pred. No. 5.3e-86		
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15144	TCCCGTGAGGCCAAATATCATTTCTGAGGGCCACAGTAATTACAACTTACTTATCGCCA	15203		
QY 61	TCCCATATACGGTATCAAACTTAGTAGAATGAAATCTGAGGAGGGTTCTCAGTAGATAAAG	120		
Db				
15204	TCCCATACATTTGGGACAGACCTAGTTCAATGAATCTGAGGAGGCTACTCAGTAGACAGTC	15263		
QY 121	CAACCCCTTACCCGATTTTTCGGCTTCACCTTTTATCCTCCATTTTATCATTTGACAGCCCTTA	180		
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15264	CCACCCCTCACAGATCTTTTACCTTTTCACTTCTCATCTTGGCCCTTCATTATTGAGGCCCTAG	15323		
QY 181	CCATAGTACACCTACTGTTTTCTCCAGAAACAGGATCCAAACCCCAACAGGAATCTCAT	240		
Db				
15324	CAACACTCCACCTCCTATTCTTGACAGAAACGGGATCAAAACAACCCCTTAGGAATCACT	15383		
QY 241	CAGACGCAGACAAAAATTCGAATCCACCCCTACTACACTATCAAGATATCCTTAGGAGCTC	300		
Db				
15384	CCCATTCGGATAAATATCACCTTCCACCCCTTATCAACAATCAAGACGCCCTCGGCTTAC	15443		
QY 301	TACTATTAAATTTTAAACCCCTCATGCTTCTAGTCTTATTTCTCACCGGACCTGCTTGGAGACC	360		
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15444	TTCTCTTCTCTCTCTCTTAATGACATTAACACTATTTCTCACAGACCTCTCTTAGCGACC	15503		
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15504	CAGACAAATATACCTTAGCCAAACCCCTTAAACACCCCTCCCAATCAAGCCCAATCAT	15563		
QY 421	ACTTCTATTGTCATACGCAATCCTCCGATCAATTTCTTAACAAACTAGGAGG	472		
Db				
15564	ATTTCCTATTTCGGCTACAAATTTCTCCGATCCGTCCCTTAAACAAACTAGGAGG	15615		

RESULT 7
US-09-377-497-7
; Sequence 7, Application US/09377497
; Patent No. 6670119
; GENERAL INFORMATION:
; APPLICANT: YOSHIKAWA, YOSHIE
; APPLICANT: MUKAI, HIROYUKI
; APPLICANT: ASADA, KIYOZO

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; APPLICANT: HINO, FUMITSUGU
; APPLICANT: KATO, IKUNOSHIN
; TITLE OF INVENTION: CANCER-ASSOCIATED GENES
; FILE REFERENCE: 1422-388P
; CURRENT APPLICATION NUMBER: US/09/377,497
; CURRENT FILING DATE: 1999-08-20
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 1140
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: any n or Xaa = unknown
US-09-377-497-7

Query Match          60.3%; Score 284.8; DB 4; Length 1140;
Best Local Similarity 75.2%; Pred. No. 4.5e-86;
Matches 355; Conservative 0; Mismatches 117; Indels 0; Gaps 0

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Qy 61 TCCCATCATCGGTACAAACCTAGTAGAATGAACTCTGGAGAGGTTCTCAGTAGATAAAG 120
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Qy 121 CAACCCCTTACCCGATTTTTCGCCCTTCACATTTATCCTCCCATTTTATCATTTGCAGGCCCTTA 180
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Qy 181 CCATAGTACACCTACTGTTCTCCACGAAACAGGATCCAAACCCCAACAGGAATCTCAT 240
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Qy 241 CAGACGAGACAAATTCATTCACCCCTACTACATATCAAAAGATATCCTTAGGAGCTC 300
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Qy 301 TACTATTAAATTTAAACCTCATGCTTCTAGTCCTATTCTCAGCGGACCTGCTTGAGACC 360
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 361 CAGACAACTATACACGACAAACCCACTTAATACACCCCCACATATCAAGGCCCGAAATGAT 420
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 421 ACTTCCTATTGGCATCGCAATCCTCCGATCAATTCCTTAACAACTAGGAGG 472
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

818 ATTTCCTATTTCGGCTACAAATTTCCGATTCGGATCCGGTCCCTTAACAACCTAGGAGG 869

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RESULT 8
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; Sequence 185, Application US/09385982
; Patent No. 6262334
; GENERAL INFORMATION:
; APPLICANT: ENDEGE, WILSON O., ET AL.
; TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
; TITLE OF INVENTION: PRODUCTS: II
; FILE REFERENCE: CCDNA-260XX
; CURRENT APPLICATION NUMBER: US/09/385,982
; CURRENT FILING DATE: 1999-08-30
; EARLIER APPLICATION NUMBER: 09/328,111
; EARLIER FILING DATE: 1999-06-08
; EARLIER APPLICATION NUMBER: 60/117,393
; EARLIER FILING DATE: 1999-01-27
; EARLIER APPLICATION NUMBER: 60/098,639
; EARLIER FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 544
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 185

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Db 301 ATACCTAGCAACCCCTTAAACACCCCTCCCAATCAAGCCGGAATGATTTCTTAT 242
QY 430 TTGCATAGCAATCTCCGATCAATTCCTTAAACAACTAGGAGG 472
Db 241 TCGCTACACAATTCTCGATCCGTCCTTAAACAGCTAGGAGG 199

RESULT 11

US-09-385-982-510/c
; Sequence 510, Application US/09385982
; Patent No. 6262334
; GENERAL INFORMATION:
; APPLICANT: ENDEGE, WILSON O., ET AL.
; TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
; FILE REFERENCE: CDNA-260XX
; CURRENT APPLICATION NUMBER: US/09/385,982
; EARLIER FILING DATE: 1999-08-30
; EARLIER FILING DATE: 1999-06-08
; EARLIER FILING DATE: 1999-01-27
; EARLIER FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 544
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 510
; LENGTH: 619
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(619)
; OTHER INFORMATION: n = A,T,C or G
US-09-385-982-510

Query Match 31.7%; Score 149.4; DB 3; Length 619;

Best Local Similarity 68.0%; Pred. No. 1.7e-40;
Matches 230; Conservative 0; Mismatches 105; Indels 3; Gaps 2;

QY 136 TTTTCGGCTTCCACTTTATCTCCCAATTATCATTTGAGCCCTTACCATAGTACACCTAC 195
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QY 196 TGTTCCTCCAGAAACAGGATCCAAACACCCACAGGAATCTCATGAGCCAGACAAA 255
Db 476 TATTTTGGCAGAAAGGATCAACCAACCCCTTAGNAATCACTTCCCATTCNGATAAA 417
QY 256 TTCCATTCACCCCTACTACACTATCAAGATATCTTAGGAGCTCTACTAATTT-TA 314
Db 416 TCACNTTCCACCTTANTACATCAAGACGCCCTCGGCTTAATTTTTTCTTCTC 357
QY 315 ACCCTCATGCTTCTAGTCCTATTCTCACCGGACCTGTGAGACCCAGACAACTATACA 374
Db 356 TCNTAATGACATTAAACATATTCTCACGACCTCTTAGGGAGCCAGACAATTAACC 297
QY 375 CAGCAAAACCCCTTAATACACCCCAATATCAAGCCCGAATGATCTTCTTATTTGCA 434
Db 296 CTAGCAACCCNTTAAACACCCCTCCCAATCAAGCCCGAATGATTTCTTATTTGCC 237
QY 435 TAGCAATCTCCGATCAATTCCTTAAACAACTAGGAGG 472
Db 236 TACAAATTCCTGATCCGTCCTTAAACAACTAGGAGG 199

RESULT 12

US-09-328-111-763/c
; Sequence 763, Application US/09328111

; Patent No. 6262333
; GENERAL INFORMATION:
; APPLICANT: ENDEGE, WILSON O.
; APPLICANT: Steinmann, Kathleen E.
; APPLICANT: Astle, Jon H.
; APPLICANT: Burgess, Christopher C.
; APPLICANT: Bushnell, Steven E.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Catino, Theodore J.
; APPLICANT: Derti, Adnan
; APPLICANT: Ford, Donna M.
; APPLICANT: Lewis, Marcia E.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
; TITLE OF INVENTION: PRODUCTS
; FILE REFERENCE: CCD-257 (US)
; CURRENT APPLICATION NUMBER: US/09/328,111
; EARLIER FILING DATE: 1999-06-08
; EARLIER APPLICATION NUMBER: US 60/088,801
; EARLIER FILING DATE: 1998-06-10
; NUMBER OF SEQ ID NOS: 850
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 763
; LENGTH: 578
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(578)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-111-763

Query Match 30.9%; Score 146; DB 3; Length 578;

Best Local Similarity 74.0%; Pred. No. 2.4e-39;
Matches 196; Conservative 0; Mismatches 68; Indels 1; Gaps 1;

QY 209 AACAGGATCCAAACACCCACAGGAATCTCATGAGCGACAGCAAAATTCATTCACCC 268
Db 569 AACGGATCAACCAACCCCTTAGGAATCACTTCCATCCGATAAATCACTTCCACCC 510
QY 269 CTACTACACTATCAAGATATCTTAGGAGCTCTAC-TATTAAATTTTAAACCTCATGCTTC 327
Db 509 TTANTACAAATCAAGACGCCCTTNGGCTTACTTCTTCTCTCTCTCTTAAATGACAT 450
QY 328 TAGTCTTATCTCAGCGAGCTGTGAGACCCAGCACTATACACCGCAACCCAC 387
Db 449 TAACACTATTCTCACCAGACCTCTAGGCGACCCAGACAAATTATACCTTAGCCAAACCCCT 390
QY 388 TTAATACACCCCAATATCAAGCCCAATGATATCTTCTTATTTGATAGCAATCTCTCC 447
Db 389 TAAACACCCCTCCCAATCAAGCCCAATGATATTTCTTATTCGCTTACCAATTTCTCC 330
QY 448 GATCAATTCCTTAAACAACTAGGAGG 472
Db 329 GATCCGTCCTTAAACAACTAGGAGG 305

RESULT 13

US-09-328-111-562/c
; Sequence 562, Application US/09328111
; Patent No. 6262333

; GENERAL INFORMATION:
; APPLICANT: ENDEGE, WILSON O.

; APPLICANT: Steinmann, Kathleen E.
; APPLICANT: Astle, Jon H.
; APPLICANT: Burgess, Christopher C.
; APPLICANT: Bushnell, Steven E.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Catino, Theodore J.
; APPLICANT: Derti, Adnan
; APPLICANT: Ford, Donna M.
; APPLICANT: Lewis, Marcia E.

APPLICANT: Monahan, John E.
APPLICANT: Schlegel, Robert
TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
FILE REFERENCE: CCD-257 (US)
CURRENT APPLICATION NUMBER: US/09/328,111
CURRENT FILING DATE: 1999-06-08
EARLIER APPLICATION NUMBER: US 60/088,801
NUMBER OF SEQ ID NOS: 850
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 562
LENGTH: 597
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)...(597)
OTHER INFORMATION: n = A,T,C or G
US-09-328-111-562

Query Match 27.6%; Score 130.4; DB 3; Length 597;
Best Local Similarity 62.8%; Pred. No. 4.5e-34;
Matches 246; Conservative 0; Mismatches 134; Indels 12; Gaps 4;

QY 93 ATCTGAGGAGGTTCTCAGTAGATAAGCAACCTTACCGGATTTTCGCC-----TT 145
DB 596 ATTTTAGGGGGTTCTCANNANACGTCCCGCCCNNTNNAAGNTTTTTNNCNCNTCAAT 537

QY 146 CCACCTTTATCTCCCATTTATCATTCAGCCCTTACCATAGTACACTACTGTTCTCCA 205
DB 536 TAAATTTGGCCNTAATATATATGNGCCNANNNGAAATTCACNTCCANTTTANGGCAN 477

QY 206 CGAAACAGGATCAACCAACCCAC--AGGAATCTCATCAGACGACGACAAATTCATTC 263
DB 476 GAAAGGGNNTCAACCAACCCCTTGNATCATCTTCCCATTCGGGATAAAATCACTTC 417

QY 264 CACCCC-TACTACTACTCAAGATATCTTAGAGCT--CTACTATTAATTTTAAACCTC 320
DB 416 CACCCCTTACTACAAATCAAGACGGCCCTCGGGCTTACTTCTCTCTCTCTCTCTTA 357

QY 321 ATGCTTCTAGTCTTCTTCTCAGCGACCTGCTTGGAGACCCAGACAACTATACACAGCA 380
DB 356 ATGACATTAACACTATCTCAGACAGCTCTTAGGCGGCCAGCAATATACCTTAGCC 297

QY 381 AACCCACTTAATACACCCCAATATCAAGCCCGAATGATCTTCTTATTTGATACGCA 440
DB 296 AACCCCTTAAACACCCCTTCCCAATCAAGCCCGAATGATATTTCTTATTCGCTACACA 237

QY 441 ATCCTCGGATCAATTCCTTAACAACTAGGAGG 472
DB 236 ATTCTCGATCGTCCCTTAAACAACTAGGAGG 205

RESULT 14
US-08-998-416-190/c
Sequence 190, Application US/08998416
Patent No. 6239264
GENERAL INFORMATION:
APPLICANT: Philippsen, Peter
APPLICANT: Pohlmann, Rainer
APPLICANT: Steiner, Sabine
APPLICANT: Mohr, Christine
APPLICANT: Wendland, Jurgon
APPLICANT: Knechtle, Philipp
APPLICANT: Reibschung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPIL
NUMBER OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 1152
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6239264artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park

STATE: No. 6239264th Carolina
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/998,416
FILING DATE: 24-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 190:
SEQUENCE CHARACTERISTICS:
LENGTH: 650 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: PAG1076RP
US-08-998-416-190

Query Match 27.1%; Score 127.8; DB 3; Length 650;
Best Local Similarity 55.2%; Pred. No. 3.5e-33;
Matches 249; Conservative 0; Mismatches 202; Indels 0; Gaps 0;

QY 1 TACCATTGAGGACAAATATCTTTTGGAGGACCAACAGTCATCACCAATCTCTTTCAGCAA 60
DB 451 TAGTATATGACAAATGTCACATGAGGTGCTACTGTATTACTAATTTATTATTAGTGCTA 392

QY 61 TCCCATACATCGGTACAAACCTAGTAGAATGAATCTGAGGAGGGTTCTCAGTAGATAAAG 120
DB 391 TTCCATTTATTGGAAATGATATTGTACTATGATGAGGATCATTTAGTGTAGTAATC 332

QY 121 CACCCCTTACCGGATTTTTCGGCTTCCACTTTTATCTCCGATTTATCATTTGAGCCCTTA 180
DB 331 CTACTATTATAAGATTTCTTTCTATTTCATTTATTAGTACCATTTATTATTGACGAATAG 272

QY 181 CCATAGTACACCTTACTGTTTCTCCAGAAACAGGATCCCAACCCACAGGAATCTCAT 240
DB 271 TAAATTAAGATTTAATGCTATTACATGATGATGTTTCAATCATCATTTAGGTATTACAG 212

QY 241 CAGACGACAGCAAAATTCATTCACCCCTTACACTATCACTATCAAAAGATATCCTTAGGAGCTC 300
DB 211 GTAAATTTAGATAGATTACCAATGCTGTTATTTTATTTTAAAGATTTAGTAACAGTAT 152

QY 301 TACTATTAAATTTTAAACCTCATGCTTCTAGTCTCTATCTCACCAGGACCTGCTTGGAGACC 360
DB 151 TTGTATTATTAATTTCTTTTCTATTATTTTGTATTTTTCACCTAATCTATTTTAGGACATC 92

QY 361 CAGACAACTATACACGACAAACCCACTTAAATACACCCCAATATCAAGCCCGAATGAT 420
DB 91 CTGATAATTATATTCAGGTAATCTCTTTAGTAGACACAGCATCTATTGTACCTGAATGAT 32

QY 421 ACTTCCTATTTCATACGCAATCTCCGATC 451
DB 31 ATTATTACCATTTCTATCTATTATTAAATC 1

RESULT 15
US-08-998-416-1032/c
Sequence 1032, Application US/08998416

Patent No. 6239264
GENERAL INFORMATION:
APPLICANT: Philippsen, Peter
APPLICANT: Pohlmann, Rainer
APPLICANT: Steiner, Sabine
APPLICANT: Mohr, Christine
APPLICANT: Wendland, Jurgen
APPLICANT: Knechtle, Philipp
APPLICANT: Reibischung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 1152
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6239264artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: No. 6239264th Carolina
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/998,416
FILING DATE: 24-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 1032:
SEQUENCE CHARACTERISTICS:
LENGTH: 716 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: PAG1631UP
US-08-998-416-1032

Query Match 27.1%; Score 127.8; DB 3; Length 716;
Best Local Similarity 55.2%; Pred. No. 3.7e-33;
Matches 249; Conservative 0; Mismatches 202; Indels 0; Gaps 0;
QY 1 TACCATGAGGCAAAATATCTTTTGGAGGAGCAACAGTCATCACCAATCTCCTTCAGCAA 60
Db 451 TAGTATATGGCAAAATGTCATTTGAGTGCTACTGTATTACTAAATTTATTAGTGCTA 392
QY 61 TCCCATACATCGGTACAAACCTAGTAGAATGAATCTGAGGAGGGTCTCTCAGTAGATAAG 120
Db 391 TTCCATTTATGGAAATGATATTTGCTATGATATGAGGATCAATTTAGTGTAGTAATC 332
QY 121 CAACCCCTTACCCGATTTTTCGCTTCCATTTATCTCCCATTTTATCATTTGACGCCCTTA 180
Db 331 CTACTATTATAAGATTTCTTCTTATTATTATTAGTACCATTATTATTATGAGCAATAG 272
QY 181 CCATAGTACACTACTGTTCTCCAGAAACAGGATCCAAACACCCACAGGATCTCAT 240
Db 271 TAAATATGCAATTTAATGCTATTATACATGATGTTTATCAATCCATTCATAGGTATTACAG 212
QY 241 CAGACGAGCAAAATTCATTTCCACCCCTACTACACTATCAAAAGATATCCTAGGAGTC 300
Db 211 GTAATTTAGATAGATTACCAATGATGGTATTATTTTAAAGATTTAGTAACAGTAT 152

QY 301 TACTATTAAATTTAAACCCCTCATGCTTCTAGTCCTATTCTCACCGGACCTGTGGAGACC 360
Db 151 TTGTATTATATAATTTCTTTTTCATATTATTGTATTCTTTTACCTTAATACTTTAGGACATC 92
QY 361 CAGACAACTATACACACGCAAAACCCACCTTAATAACACCCCAATATCAAGCCCGAATGAT 420
Db 91 CTGATAATTAATATCCAGGTAATCCTTTAGTAACACACGACATCTATTGTACCTGAATGAT 32
QY 421 ACTTCCTATTGTCATACGCAATCTCCGATC 451
Db 31 ATTTATTACCAATCTATCTTATTATTTAAAGATC 1

Search completed: November 17, 2004, 03:15:13
Job time : 169.862 secs

[illegible]

Query Match	67.5%;	Score 318.4;	DB 16;	Length 16300;
Best Local Similarity	79.7%;	Pred. No. 1.2e-88;		

QY 235 TCTCATGAGCCAGCAAAATTCATTCACCCCTACTACACTATCAAGATATCTTAG 294
Db 181 TTCTCTCAGAGTAGACAAATCCCAATCCACCCCTACTATACCAATTAAGGACATCTTAG 240
QY 295 GAGCTCTACTATTAATTTTAAACCTCATGCTTCTAGTCTTCTATTCACCGGACCTGCTTG 354
Db 241 GGGCCCTCTTACTAATCTTAGCTCTAATCTACTAGTACTATTCGACCCCGACCTCTCTG 300
QY 355 GAGACCCAGACAACTATACACAGCAAAACCCCACTTAATATACACCCCAATATCAAGCCCG 414
Db 301 GAGACCCAGATAAATACACCCCGCAATCCCACTCAACACACCCCTCACATCAAAACCG 360
QY 415 AATGATACTCTTATTCATGACGCAATCTCGATCAATCTTCACTAACTAGGA 470
Db 361 AGTGATACTCTTATTTGATACGCAATCTTAGATCAATCGCCCAACANACTAGGA 416

RESULT 4
US-09-960-352-3407
; Sequence 3407, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 3407
; LENGTH: 411
; TYPE: DNA
; ORGANISM: Bos taurus
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (289)
; OTHER INFORMATION: unsure at all n locations
; OTHER INFORMATION: Clone ID: 15-LIB34-003-Q1-E1-D11
US-09-960-352-3407

Query Match 65.3%; Score 308.2; DB 9; Length 411;
Best Local Similarity 84.4%; Pred. No. 3.6e-86;
Matches 346; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 6 TGAGGACAAATATCTTTTGGAGGACCAACAGTCAACCAATCTCTTTTTCAGCAATCCCA 65
Db 1 TGAGGACAAATATCAITCTGAGGAGCAACAGTCAACCAATCTCTTTTTCAGCAATCCCA 60
QY 66 TACATCGGTACAAACCTAGTAGAATGAATCTGAGGAGGTTCTCAGTAGAATAAGCAAC 125
Db 61 TACATCGGCACAAATTAGTTCGAATGAATCTGAGGCGGATTTCTCAGTAGAATAAGCAAC 120
QY 126 CTTACCGGATTTTTCGCTTCCATTTATCTCCGATTTATCTCAGTTCAGGCGCTTACATA 185
Db 121 CTTACCGGATTTTTCGCTTCCATTTTATCTCTTCCATTTATCTCAGTTCAGGCGCTTACATA 180
QY 186 GTACACTACTGTTTCTCCAGCAAAACAGGATCAACCAACCCCAAGAAATCTCATCAGAC 245
Db 181 GTCCACTACTATTTCTCCAGCAAAACAGGCTCAACCAACCCCAAGAAATTTCTCAGAC 240
QY 246 GCAGACAAATTCATTCACCCCTACTACACTATCAAGATATCTTAGGAGCTCTACTA 305
Db 241 GTAGACAAATTCATTCACCCCTACTATACCAATTAAGGACATCTTAGGCGCTCTTA 300
QY 306 TTAATTTAAACCTCATGCTTCTAGTCTTATCTCAGGAGACCTGCTTGAGACCCAGAC 365
Db 301 CTAATTTAGTCTTAATACTACTAGTACTATTCGACCCGACCTCTCTCGGAGACCCAGAT 360
QY 366 AACTATACACCAACCAACCTTAATATACACCCCAACATATCAAGCCGA 415

Db 361 AACTATACCCAGCAATTCCTCACTCAACACACCCCTCTCATCAACACCGGA 410

RESULT 5
US-09-960-352-9822
; Sequence 9822, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 9822
; LENGTH: 412
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 42-LIB34-012-Q1-E1-C10
US-09-960-352-9822

Query Match 65.3%; Score 308; DB 9; Length 412;
Best Local Similarity 84.2%; Pred. No. 4.1e-86;
Matches 347; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

QY 36 GTCATCAACCAATCTCTTTTTCAGCAATCCCATACATCGGTACAAACCTAGTAGAATGAATC 95
Db 1 GTCATCAACCAATCTCTTTTTCAGCAATCCCATACATCGGTACAAACCTAGTAGAATGAATC 60
QY 96 TGAGGAGGTTCTCAGTAGATAAAGCAACCTTACCCGATTTTTCGCTTCCACTTTATC 155
Db 61 TGAGGCGGATTTCTCAGTAGATAAAGCAACCTTACCCGATTTTTCGCTTCCACTTTATC 120
QY 156 CTCCCATTTATCATTCGAGCCCTTACCATAGTACACTACTGTTCTCCAGCAAAACAGGA 215
Db 121 CTTCATTTTATCATCATAGCAATTTGCCATAGTCCACTACTATTTCTCCAGCAAAACAGGC 180
QY 216 TCCACAAACCCCAACAGGAATCTCATCAGACGAGCAAAATTCATTCACCCCTACTAC 275
Db 181 TCCACAAACCCCAACAGGAATTTCTTCAGAGTAGACAAATTCATTCACCCCTACTAT 240
QY 276 ACTATCAAGATATCTCAGGAGTCTACTATTAATTTTAACTTAACTTCTAGTCTTA 335
Db 241 ACCATTAAAGGACATCTTAGGGGCTCTTTACTAAATTTAGTCTTAATCTAGTACTA 300
QY 336 TTCTCAGCGGACCTGCTTCGAGACCCAGCAACTATACACCAACCAACCACTTAATACA 395
Db 301 TTGCGACCCGACCTCTCTCGAGACCCAGCAACTATACACCCAGCAACTTCACTCAACA 360
QY 396 CCCCCACATATCAAGCCCGAATGATCTTCTTATTTGATACGCAATCTCTCC 447
Db 361 CCCCCACATCAAAACCCGAGTACTTCTTATTTGATACGCAATCTTAC 412

RESULT 6
US-09-960-352-8757
; Sequence 8757, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24

```
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 8757
; LENGTH: 448
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 38-BOVMS1-021-Q1-E1-B6
US-09-960-352-8757

Query Match      63.9%; Score 301.6; DB 9; Length 448;
Best Local Similarity 84.2%; Pred. No. 4.4e-84;
Matches 340; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

Qy 69 ATCGGTACAAACCTAGTAGAATGAATCTGAGGAGGGTCTCAGTAGATAAAGCAACCCCTT 128
Db 1 ATCGGCACAAATTTAGTCGAATGAATCTGAGGCGAATCTCAGTAGACAAAGCAACCCCTT 60

Qy 129 ACCGATTTTTCGCTTCCCATTTATCTCTCCATTTATCATTTGCGAGCCCTTACCATAGTA 188
Db 61 ACCGATTTTTCGCTTCCCATTTATCTCTCCATTTATCATCATAGCAATTTGCCATAGTC 120

Qy 189 CACCTACTGTTTCTCCAGAAACAGGATCCCAACACCCACAGGAATCTCATCAGAGCA 248
Db 121 CACCTACTATTTCTCCAGAAACAGGCTCCCAACACCCACAGGAATTTCTCAGAGCA 180

Qy 249 GACAAAATTCATTTCCACCCCTACTACACTATCAAGATATCTTAGGAGCTCTACTATTA 308
Db 181 GACAAAATTCATTTCCACCCCTACTATACCATTAAGGACATCTTAGGGCCCTCTTACTA 240

Qy 309 ATTTTAACCCCTCATGCTTCTAGTCTTATCTCAGGAGACCTGTTGGAGACCCAGACAAC 368
Db 241 ATTCTAGCTCTTAATACTACTAGTACTATTGCAACCCGACCTCTCGGAGACCCAGATAAC 300

Qy 369 TATACACAGCAAAACCCACTTAATACACCCCAATATCAAGCCCGAATGATCTTCTTA 428
Db 301 TACACCCGAGCAATCACTACACACACCCCTCATATCAACCAACCCGAGTATCTTCTTA 360

Qy 429 TTGTCATACGCAATCTCCGATCAATTTCTTAACAAACTAGGAGG 472
Db 361 TTGTCATACGCAATCTTACGATCAATCCCAACAAACTAGGAGG 404

RESULT 7
US-10-308-264-370
; Sequence 370, Application US/10308264
; Publication No. US20040029133A1
; GENERAL INFORMATION:
; APPLICANT: Herrnstadt, Corinna
; TITLE OF INVENTION: MITOCHONDRIAL DNA POLYMORPHISM
; FILE REFERENCE: 660088.461
; CURRENT APPLICATION NUMBER: US/10/308,264
; CURRENT FILING DATE: 2002-11-25
; NUMBER OF SEQ ID NOS: 697
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 370
; LENGTH: 16565
; <211> conflict
; TYPE: DNA
; ORGANISM: Homo sapiens mitochondrial
; FEATURE:
; LOCATION: 3110
; OTHER INFORMATION: "n" refers to a nucleotide at position 3107 of the
; OTHER INFORMATION: Cambridge Reference Sequence (CRS, Anderson et al.
; OTHER INFORMATION: 1981 Nature 290:457-465), later determined to be
; OTHER INFORMATION: absent from the human mtDNA sequence according to
; OTHER INFORMATION: the revised CRS (rCRS, Andrews et al. 1999 Nature
; OTHER INFORMATION: Genetics 23:147); "n" therefore represents a
; OTHER INFORMATION: single nucleotide deletion at a position corresponding to
; OTHER INFORMATION: nucleotide 3107 of SEQ ID NO:1 as provided herein.
US-10-308-264-370

Query Match      61.0%; Score 288; DB 16; Length 16565;
Best Local Similarity 75.6%; Pred. No. 4.1e-79;
Matches 357; Conservative 0; Mismatches 115; Indels 0; Gaps 0;

Qy 1 TACCATGAGGACAAATATCTTTTGGAGGACCAAGTCAATCACCNAATCTCTTTTCAGCAA 60
Db 15138 TCCGTGAGGCCAAATATCATTTCTGAGGGGCCACAGTAATTAACAACCTTACTATCCGCCA 15197

Qy 61 TCCCATACATCGGTACAAACCTAGTAGAATGAATCTGAGGAGGGTCTCAGTAGATAAAG 120
Db 15198 TCCCATACATTTGGGACAGACCTAGTTCAATGAATCTGAGGAGGCTACTCAGTAGACAGTC 15257

Qy 121 CAACCCCTTACCCGATTTTTCGCTTCCCACTTTATCTCTCCCAATTTATCATTTGACGCCCTTA 180
Db 15258 CCACCCCTCACAGGATTTCTTTACCTTTCACCTTCATCTTTCGCTTCTCATTTATGAGCCCTAG 15317

Qy 181 CCATAGTACACCTACTGTTTCTCCAGAAACAGAGATCCAAACCCACAGGAATCTCAT 240
Db 15318 CAGCACTCCACCTCTTATTTCTGACGAAACGGGATCAAAACGCCCTTAGGAATCACCT 15377

Qy 241 CAGACGAGACAAATTTCCATTTCCACCCCTACTACACTATCAAGATATCTCTAGGAGCTC 300
Db 15378 CCCATTCGACAAATTCACCTTCCACCTTACTACAAATCAAGACGCCCTCGGCTTAC 15437

Qy 301 TACTATTAATTTTAAACCCCTCATGCTTCTAGTCTTATTTCTACCGGACCTGCTTGGAGACC 360
Db 15438 TTCTCTTCTCTCTCTCTCTTAATGACATTAACACTATTCTCACCAGACCTCTAGGCGACC 15497

Qy 361 CAGCAACTATACACCGACCAACCCACTTAATACACCCCAATATCAAGCCCGAATGAT 420
Db 15498 CAGCAATATATACCTTAGCCCAACCCCTTAAATATCCCTTCCCTTACAACTAGGAGG 15557

Qy 421 ACTTCTTATTTGCAATGCGCAATCTCCGATCAATTTCTTAAACAACTAGGAGG 472
Db 15558 ATTCTCTATTCTGCTACACAAATTTCTCGATCCGCTTCCCTTACAACTAGGAGG 15609

RESULT 8
US-10-308-264-479
; Sequence 479, Application US/10308264
; Publication No. US20040029133A1
; GENERAL INFORMATION:
; APPLICANT: Herrnstadt, Corinna
; TITLE OF INVENTION: MITOCHONDRIAL DNA POLYMORPHISM
; FILE REFERENCE: 660088.461
; CURRENT APPLICATION NUMBER: US/10/308,264
; CURRENT FILING DATE: 2002-11-25
; NUMBER OF SEQ ID NOS: 697
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 479
; LENGTH: 16569
; <211> conflict
; TYPE: DNA
; ORGANISM: Homo sapiens mitochondrial
; FEATURE:
; LOCATION: 3107
; OTHER INFORMATION: "n" refers to a nucleotide at position 3107 of the
; OTHER INFORMATION: Cambridge Reference Sequence (CRS, Anderson et al.
; OTHER INFORMATION: 1981 Nature 290:457-465), later determined to be
; OTHER INFORMATION: absent from the human mtDNA sequence according to
; OTHER INFORMATION: the revised CRS (rCRS, Andrews et al. 1999 Nature
; OTHER INFORMATION: Genetics 23:147); "n" therefore represents a
; OTHER INFORMATION: single nucleotide deletion at a position corresponding to
; OTHER INFORMATION: nucleotide 3107 of SEQ ID NO:1 as provided herein.
US-10-308-264-479

Query Match      61.0%; Score 288; DB 16; Length 16569;
Best Local Similarity 75.6%; Pred. No. 4.1e-79;
Matches 357; Conservative 0; Mismatches 115; Indels 0; Gaps 0;

Qy 1 TACCATGAGGACAAATATCTTTTGGAGGACCAAGTCAATCACCNAATCTCTTTTCAGCAA 60
Db 15144 TCCGTGAGGCCAAATATCATTTCTGAGGGGCCACAGTAATTAACAATTAATTAATCCGCCA 15203

Qy 61 TCCCATACATCGGTACAAACCTAGTAGAATGAATCTGAGGAGGGTCTCAGTAGATAAAG 120
Db 15144 TCCGTGAGGCCAAATATCATTTCTGAGGGGCCACAGTAATTAACAATTAATTAATCCGCCA 15203
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QY 301 TACTATTAAATTTTAAACCCCTCATGCTTCTAGTCTTATTCTACCGGACCTGCTTGAGACC 360
Db 15447 TTCTCTTCTCTCTCTTAATGACATTAACACTATTCTCACCAGACCTCTTAGCGACC 15506
QY 361 CAGACAACTATACACAGCAAAACCCACTTATATACACCCCCACATATCAAGCCCGAATGAT 420
Db 15507 CAGACAAATATACCCCTAGCCAAACCCCTTAAACACACCCCTCCACATCAAGCCCGAATGAT 15566
QY 421 ACTTCCTATTGTCATACCAATCTCCGATCAATTCCTTAACAAACTAGGAGG 472
Db 15567 ATTTCCTATTGCTTACCAATTCCTCCGATCGTCCCTTAAACAAACTAGGAGG 15618

RESULT 11
US-10-308-264-150
; Sequence 150, Application US/10308264
; Publication No. US20040029133A1
; GENERAL INFORMATION:
; APPLICANT: HerinStadt, Corinna
; TITLE OF INVENTION: MITOCHONDRIAL DNA POLYMORPHISM
; FILE REFERENCE: 660088.461
; CURRENT APPLICATION NUMBER: US/10/308,264
; CURRENT FILING DATE: 2002-11-25
; NUMBER OF SEQ ID NOS: 697
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 150
; LENGTH: 16559
; <211> conflict
; TYPE: DNA
; ORGANISM: Homo sapiens mitochondrial
; FEATURE:
; LOCATION: 3106
; OTHER INFORMATION: "n" refers to a nucleotide at position 3107 of the
; OTHER INFORMATION: Cambridge Reference Sequence (CRS, Anderson et al.
; OTHER INFORMATION: 1981 Nature 290:457-465), later determined to be
; OTHER INFORMATION: absent from the human mtDNA sequence according to
; OTHER INFORMATION: the revised CRS (rCRS, Andrews et al. 1999 Nature
; OTHER INFORMATION: Genetics 23:147); "n" therefore represents a
; OTHER INFORMATION: single nucleotide deletion at a position corresponding to
; OTHER INFORMATION: nucleotide 3107 of SEQ ID NO:1 as provided herein.
US-10-308-264-150

Query Match 60.7%; Score 286.4; DB 16; Length 16559;
Best Local Similarity 75.4%; Pred. No. 1.3e-78;
Matches 356; Conservative 0; Mismatches 116; Indels 0; Gaps 0;

QY 1 TACCATGAGGCAAAATATCTTTTGGAGGAGCAACAGTCATCAACCAATCTCTTTAGCAA 60
Db 15134 TCCCGTAGGGCCAAATATCATCTCTGAGGGGCCACAGTAATTACAAACTTACTATCCGCCA 15193
QY 61 TCCCATACATCGGTACAAACCTAGTAGAATGAATCTGAGGAGGTTCTCTAGTAGATAAAG 120
Db 15194 TCCCATACATTTGGACAGACCTAGTTCATGAATCTGAGGAGGCTACTCAGTAGACAGTC 15253
QY 121 CAACCCCTTACCGGATTTTTCGCTTCCACTTTATCTCTCCCATTTATCATTTGACGCCCTTA 180
Db 15254 CCACCCCTCACAGGATCTTTTACCTTTTCACTTCATCTTGCCCTTCATTTTGCAGCCCTAG 15313
QY 181 CCATAGTACACCTACTGTTTCCACGAAACAGGATCCAAACCCACAGGATCTCAT 240
Db 15314 CAGCACTCCACCTCTATTTTGCAGAAACGGGATCAAAACACCCCTAGGATCACCT 15373
QY 241 CAGACGAGACAAATTCCTTCCACCCCTACTACACTATCAAGATATCTAGGAGCTC 300
Db 15374 CCATTCGGATAAATCACCTTCCACCTTACTACAAATCAAGAGCGCCTCGGCTTAC 15433
QY 301 TACTATTAAATTTTAAACCCCTCATGCTTCTAGTCTTATTCTCACCAGGACCTCTTGAGACC 360
Db 15434 TTCTCTTCTCTCTCTTAATGACATTTTCCGATCGTCCCTTAAACAACTAGGAGG 15493
QY 421 CAGACAACTATACACAGCAAAACCCACTTAAATACACCCCAATATCAAGCCCGAATGAT 420
Db 15494 CAGACAAATATACCCCTAGCCAAACCCCTTAAACACCCCTCCACATCAAGCCCGAATGAT 15553

US-10-308-264-150

Query Match 60.7%; Score 286.4; DB 16; Length 16559;
Best Local Similarity 75.4%; Pred. No. 1.3e-78;
Matches 356; Conservative 0; Mismatches 116; Indels 0; Gaps 0;

QY 1 TACCATGAGGCAAAATATCTTTTGGAGGAGCAACAGTCATCAACCAATCTCTTTAGCAA 60
Db 15134 TCCCGTAGGGCCAAATATCATCTCTGAGGGGCCACAGTAATTACAAACTTACTATCCGCCA 15193
QY 61 TCCCATACATCGGTACAAACCTAGTAGAATGAATCTGAGGAGGTTCTCTAGTAGATAAAG 120
Db 15194 TCCCATACATTTGGACAGACCTAGTTCATGAATCTGAGGAGGCTACTCAGTAGACAGTC 15253
QY 121 CAACCCCTTACCGGATTTTTCGCTTCCACTTTATCTCTCCCATTTATCATTTGACGCCCTTA 180
Db 15254 CCACCCCTCACAGGATCTTTTACCTTTTCACTTCATCTTGCCCTTCATTTTGCAGCCCTAG 15313
QY 181 CCATAGTACACCTACTGTTTCCACGAAACAGGATCCAAACCCACAGGATCTCAT 240
Db 15314 CAGCACTCCACCTCTATTTTGCAGAAACGGGATCAAAACACCCCTAGGATCACCT 15373
QY 241 CAGACGAGACAAATTCCTTCCACCCCTACTACACTATCAAGATATCTAGGAGCTC 300
Db 15374 CCATTCGGATAAATCACCTTCCACCTTACTACAAATCAAGAGACCCCTCGGCTTAC 15433
QY 301 TACTATTAAATTTTAAACCCCTCATGCTTCTAGTCTTATTCTCACCAGGACCTCTTGAGACC 360
Db 15434 TTCTCTTCTCTCTCTTAATGACATTTTCCGATCGTCCCTTAAACAACTAGGAGG 15493
QY 421 CAGACAACTATACACAGCAAAACCCACTTAAATACACCCCAATATCAAGCCCGAATGAT 420
Db 15494 CAGACAAATATACCCCTAGCCAAACCCCTTAAACACCCCTCCACATCAAGCCCGAATGAT 15553
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QY 421 ACTTCCTATTGTCATACCAATCTCCGATCAATTCCTTAACAAACTAGGAGG 472
Db 15554 ATTTCCTATTGCTTACCAATTCCTCCGATCGTCCCTTAAACAAACTAGGAGG 15605

RESULT 12
US-10-308-264-214
; Sequence 214, Application US/10308264
; Publication No. US20040029133A1
; GENERAL INFORMATION:
; APPLICANT: HerinStadt, Corinna
; TITLE OF INVENTION: MITOCHONDRIAL DNA POLYMORPHISM
; FILE REFERENCE: 660088.461
; CURRENT APPLICATION NUMBER: US/10/308,264
; CURRENT FILING DATE: 2002-11-25
; NUMBER OF SEQ ID NOS: 697
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 214
; LENGTH: 16559
; <211> conflict
; TYPE: DNA
; ORGANISM: Homo sapiens mitochondrial
; FEATURE:
; LOCATION: 3106
; OTHER INFORMATION: "n" refers to a nucleotide at position 3107 of the
; OTHER INFORMATION: Cambridge Reference Sequence (CRS, Anderson et al.
; OTHER INFORMATION: 1981 Nature 290:457-465), later determined to be
; OTHER INFORMATION: absent from the human mtDNA sequence according to
; OTHER INFORMATION: the revised CRS (rCRS, Andrews et al. 1999 Nature
; OTHER INFORMATION: Genetics 23:147); "n" therefore represents a
; OTHER INFORMATION: single nucleotide deletion at a position corresponding to
; OTHER INFORMATION: nucleotide 3107 of SEQ ID NO:1 as provided herein.
US-10-308-264-214

Query Match 60.7%; Score 286.4; DB 16; Length 16559;
Best Local Similarity 75.4%; Pred. No. 1.3e-78;
Matches 356; Conservative 0; Mismatches 116; Indels 0; Gaps 0;

QY 1 TACCATGAGGCAAAATATCTTTTGGAGGAGCAACAGTCATCAACCAATCTCTTTAGCAA 60
Db 15134 TCCCGTAGGGCCAAATATCATCTCTGAGGGGCCACAGTAATTACAAACTTACTATCCGCCA 15193
QY 61 TCCCATACATCGGTACAAACCTAGTAGAATGAATCTGAGGAGGTTCTCTAGTAGATAAAG 120
Db 15194 TCCCATACATTTGGACAGACCTAGTTCATGAATCTGAGGAGGCTACTCAGTAGACAGTC 15253
QY 121 CAACCCCTTACCGGATTTTTCGCTTCCACTTTATCTCTCCCATTTATCATTTGACGCCCTTA 180
Db 15254 CCACCCCTCACAGGATCTTTTACCTTTTCACTTCATCTTGCCCTTCATTTTGCAGCCCTAG 15313
QY 181 CCATAGTACACCTACTGTTTCCACGAAACAGGATCCAAACCCACAGGATCTCAT 240
Db 15314 CAGCACTCCACCTCTATTTTGCAGAAACGGGATCAAAACACCCCTAGGATCACCT 15373
QY 241 CAGACGAGACAAATTCCTTCCACCCCTACTACACTATCAAGATATCTAGGAGCTC 300
Db 15374 CCATTCGGATAAATCACCTTCCACCTTACTACAAATCAAGAGCGCCTCGGCTTAC 15433
QY 301 TACTATTAAATTTTAAACCCCTCATGCTTCTAGTCTTATTCTCACCAGGACCTCTTGAGACC 360
Db 15434 TTCTCTTCTCTCTCTTAATGACATTTTCCGATCGTCCCTTAAACAACTAGGAGG 15493
QY 421 ACTTCCTATTGTCATACCAATCTCCGATCAATTCCTTAACAAACTAGGAGG 472
Db 15554 ATTTCCTATTGCTTACCAATTCCTCCGATCGTCCCTTAAACAAACTAGGAGG 15605

RESULT 13
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RESULT 14
US-10-308-264-373
: Sequence 373, Application US/10308264
: Publication No. US20040029133A1
: GENERAL INFORMATION:
: APPLICANT: HerinStadt, Corinna
: TITLE OF INVENTION: MITOCHONDRIAL DNA POLYMORPHISM
: FILE REFERENCE: 660088.461

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; TYPE: DNA
; ORGANISM: Homo sapiens mitochondrial
; FEATURE:
; LOCATION: 3108
; OTHER INFORMATION: "n" refers to a nucleotide at position 3107 of the
; Cambridge Reference Sequence (CRS, Anderson et al.
; 1981 Nature 290:457-465), later determined to be
; absent from the human mtDNA sequence according to
; the revised CRS (rCRS, Andrews et al. 1999 Nature
; Genetics 23:147); "n" therefore represents a
; single nucleotide deletion at a position corresponding to
; nucleotide 3107 of SEQ ID NO:1 as provided herein.
US-10-308-264-206

Query Match      60.7%; Score 286.4; DB 16; Length 16561;
Best Local Similarity 75.4%; Pred. No. 1.3e-78;
Matches 356; Conservative 0; Mismatches 116; Indels 0; Gaps 0;

Qy 1 TACCATGAGGCAAAATATCTTTTTCAGGAGCAACAGTCATCACCAAATCTCCTTTTCAGCAA 60
Db 15136 TCCCGTGAGGCCAAATATCATCTGAGGGGCCACAGTAATTACAAACTTACTATCCGCCA 15195

Qy 61 TCCCATACATCGGTACAAACCTAGTAGAATGAATCTGAGGAGGGTTCTCAGTAGATAAAG 120
Db 15196 TCCCATACATTTGGGACAGACCTAGTTCAATGAATCTGAGGAGGCTACTCAGTAGACAGTC 15255

Qy 121 CAAGCCTTACCCGATTCTTCGCTTCCACCTTTATCTCCCATTTATCATTTGCAGCCCTTA 180
Db 15256 CCACCTTCACAGGATCTTTACCTTCACTTCTGCCCCTTCAATTATTCAGCCCTTAG 15315

Qy 181 CCATAGTACACTACTGTGTTCTCCACGAAACAGGATCCAAACCCCAACAGGAATCTCAT 240
Db 15316 CAGCACTCCACCTCCTATTTCTTTCAGGAAACGGGATCAACACACCCCTAGGAATCACT 15375

Qy 241 CAGAGCGAGACAAATTCATTCACCCCTACTACATATCAAGATATCCTAGGAGCTC 300
Db 15376 CCCATTCCGATAAAATCACTTCCACCCCTTACTACAAATCAAGAGCCCTCGGCTTAC 15435

Qy 301 TACTATTAAATTTAACCCCTCATGCTTCTAGTCTTATCTACCGGACCTGCTTGGAGACC 360
Db 15436 TTCTCTTCCCTTCTCTCCTTAATGACATTAACACTATTCTACAGACCTCCTAGGAGACC 15495

Qy 361 CAGACAATATACCCAGCAACCCACTTAAATACACCCCAATATCAAGCCCGAATGAT 420
Db 15496 CAGACAATATACCCAGCAACCCCTTAAATACCCCTCCCAATCAAGCCCGAATGAT 15555

Qy 421 ACTTCCTATTTGCATACGCAATCTCCGATCAATTCCTAACAACTAGGAGG 472
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Search completed: November 17, 2004, 03:11:54
Job time : 706.939 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 16, 2004, 22:24:28 ; Search time 6487.97 Seconds
(without alignments)
2650.992 Million cell updates/sec

Title: US-09-821-782E-48
Perfect score: 472
Sequence: 1 taccatgggacaaatatct.....attcctaacaactaggagg 472

Scoring table: IDENTITY_NDC
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST: *
1: gb_est1: *
2: gb_est2: *
3: gb_hic: *
4: gb_est3: *
5: gb_est4: *
6: gb_est5: *
7: gb_est6: *
8: gb_gss1: *
9: gb_gss2: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	362.2	76.7	840	7	CF614528	CES008735
3	362	76.7	840	7	CN822842	Oa splbn
4	361.6	76.6	571	4	BG689885	338199 BA
5	361.6	76.6	574	6	CB220822	1AB026G11
6	361.6	76.6	692	6	CB449349	703541 MA
7	361.6	76.6	727	6	CB444500	695671 MA
8	361.6	76.6	728	6	CB439091	688000 MA
9	359	76.1	863	7	CN824188	Oa splbn
10	355.6	75.3	515	6	CB223436	1JEJ23E10
11	355.6	75.3	552	6	CB220605	1AB024C06
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13	355	75.2	648	7	CN789904	4124424 B
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15	353.6	74.9	487	4	BM434623	1R11A03
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17	351	74.4	610	6	CB537456	775083 MA
18	350.6	74.3	575	2	BB590256	197290 BA
19	350.6	74.3	664	1	AV610345	AV610345
20	350.6	74.3	670	6	CB449447	703648 MA
21	350	74.2	462	6	CB536710	771751 MA
22	350	74.2	729	6	CB454877	711703 MA
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33	331.2	70.2	830	7	CN155599	
34	331.2	70.2	880	7	CN003411	
35	331.2	70.2	887	7	CK454695	
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39	328.8	69.7	629	7	CF615029	
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41	326.4	69.2	764	4	BI817190	
42	326.2	69.1	705	6	CB447959	
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ALIGNMENTS

RESULT 1
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LOCUS
DEFINITION
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803 bp mRNA linear EST 02-JUN-2004
ACCESSION
CN822665
VERSION
CN822665.1 GI:47950734
KEYWORDS
EST.
SOURCE
Ovis aries (sheep)
ORGANISM
Ovis aries
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Caprinae; Ovis.
REFERENCE
1 (bases 1 to 803)
Gosner,A. and Hopkins,J.
Ovine spleen/brain cdna library
TITLE
Unpublished (2004)
JOURNAL
COMMENT
Contact: J Hopkins
Veterinary Biomedical Sciences
University of Edinburgh
Summerhall Square, Edinburgh, EH9 1QH.
Email: j.hopkins@ed.ac.uk
Plate: 02 row: O column: 17
Seq primer: M13reverse
High quality sequence start: 6
High quality sequence stop: 549.
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Matches 407; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

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Db	87	TACCATGAGGACAAATATCTTTTGAGGAGCAACAGTCATCACAAATCTCTTTCAGCAA	146
Qy	61	TCCCATACATCGGTACAACTAGTAGAATCTCAGGAGGTTCTCAGTAGATAAAG	120
Db	147	TTCCATATATTGGCACAAACCTAGTCGAATCTGGGGAGGATTCCTAGTAGACAAG	206

ORIGIN

Query Match 76.7%; Score 362.2; DB 7; Length 670;
Best Local Similarity 85.4%; Pred. No. 1.9e-95;
Matches 403; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

FEATURES	source
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Caprinae; Ovis.
1 (bases 1 to 840)
Gossner, A. and Hopkins, J.
Ovine spleen\brain CDNA library
Unpublished (2004)
Contact: J Hopkins
Veterinary Biomedical Sciences
University of Edinburgh
Summerhall Square, Edinburgh, EH9 1QH.
Email: j.hopkins@ed.ac.uk
Plate: 02 row: G column: 06
Seq primer: M13reverse
High quality sequence start: 5
High quality sequence stop: 549.

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FEATURES
source

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I; Site 2: Xho I"

ORIGIN

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Best Local Similarity 85.4%; Pred. No. 2.8e-95;
Matches 403; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

Qy 1 TACCATGAGGACAAATATCTTTTGGAGGACCAAGTCATCACCACCTCTCTTTTCAGCAA 60
Db 21 TACCATGAGGACAAATATCAATCTGAGGACCAAGTCATCACCACCTCTTTTCAGCAA 80
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Db 81 TCCCATACATCGGCACAAATTTAGTCGAATGAATCTGAGGCGGATTTCTCAGTAGACAAAG 140
Qy 121 CAACCCCTTACCCGATTTTTCGCTTCCACTTTATCTCTCCCTTTATCATTCAGCGCCCTTA 180
Db 141 CAACCCCTTACCCGATTTCTGCTTTCCATTTATCTCTCTTCCATTTATCATCATAGCAATG 200
Qy 181 CCATAGTACACTACTGTTTCTCCAGAAACAGAGTCCAAACCCCAACAGGAATCTCAT 240
Db 201 CCATAGTCCACTACTATTTCTCCAGAAACAGAGTCCAAACCCCAACAGGAATTTTCT 260
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Db 261 CAGAGGAGACAAATTCATTCACCCCTTACTACACTATCAAGATATCTTAGAGGTC 320
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Qy 361 CAGACACTATACACGAGCAACCCATTAATACACCCCAATATCAAGCCCAAGTAT 420
Db 381 CAGATAACTACACCCGCAATCCACTCAACACACCCCTCATCAATCAACCCGAGTAT 440
Qy 421 ACTTCTATTGTCATGCAATCTCTCGCATCAATTTCTTAACAACCTAGGAG 472
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RESULT 6

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LOCUS
DEFINITION 703541 MARC 6BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION CB449349
VERSION
KEYWORDS EST.
SOURCE
ORGANISM Bos taurus (cow)

REFERENCE

AUTHORS Smith, T.P.L., Roberts, A.J., Echtenkamp, S.E., Chitko-McKown, C.G., Wray, J.E. and Keele, J.W.
TITLE A second set of bovine ESTs from pooled-tissue normalized libraries
JOURNAL Unpublished (2003)
COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390

Email: smith@mail.marc.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and trimmed with the aid of the trim_alt option. Vector identified with cross_match v0.990329.
Plate: FQY8059 row: L column: 22
Seq primer: GTAATACGACTCACTATAGG.
Location/Qualifiers

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source

1. .692
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Library made with RNA pooled from multiple tissues
including liver, lung, hypothalamus, pituitary, and
placenta/endometrium."

ORIGIN

Query Match 76.6%; Score 361.6; DB 6; Length 692;
Best Local Similarity 85.4%; Pred. No. 2.9e-95;
Matches 403; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

Qy 1 TACCATGAGGACAAATATCTTTTGGAGGACCAAGTCATCACCACCTCTCTTTTCAGCAA 60
Db 16 TACCATGAGGACAAATATCAATCTGAGGACCAAGTCATCACCACCTCTTTTCAGCAA 75
Qy 61 TCCCATACATCGGTACCAACCTAGTAGAATGAATCTGAGGAGGTTCTCAGTAGATAAAG 120
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RESULT 7

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LOCUS
DEFINITION 695671 MARC 6BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION CB444500
VERSION
KEYWORDS EST.
SOURCE
ORGANISM Bos taurus (cow)

REFERENCE
AUTHORS Smith, T.P.L., Roberts, A.J., Echtenkamp, S.E., Chitko-McKown, C.G., Wray, J.E. and Keele, J.W.
TITLE A second set of bovine ESTs from pooled-tissue normalized libraries

JOURNAL COMMENT

Unpublished (2003)
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and trimmed with the aid of the trim_alt option. Vector identified with cross_match v0.990329.
Plate: FQY8052 row: H column: 9
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Location/Qualifiers

FEATURES

source

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ORIGIN

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Best Local Similarity 85.4%; Pred. No. 3e-95;
Matches 403; Conservative 0; Mismatches 69; Indels 0; Gaps 0;
QY 1 TACCATGAGGACAAATATCTTTTGGAGGACACAGTCATCACCAATCTCTTCAGCAA 60
Db 60 TACCATGAGGACAAATATCTTTTGGAGGACACAGTCATCACCAATCTTTATCAGCAA 119
QY 61 TCCCATACATCGGTACAAACCTAGTAGAATGAATCTGAGGAGGTTCTCAGTAGATAAAG 120
Db 120 TCCCATACATCGGCACAAATTTAGTCGAATGAATCTGAGGCGGATTCTCAGTAGACAAAG 179
QY 121 CAACCTTACCCGATTTTCGCCTTCACATTTTATCTCCATTTATCATTCGACGCCCTTA 180
Db 180 CAACCTTACCCGATTTTCGCCTTCACATTTTATCTCCATTTATCATTCATGCAATG 239
QY 181 CCATAGTACACCTACTGTTTCTCCAGAAACAGATCCCAACCCACACAGGAATCTCAT 240
Db 240 CCATAGTACACCTACTGTTTCTCCAGAAACAGATCCCAACCCACACAGGAATTTCT 299
QY 241 CAGACGAGACAAATTCATTCACCCCTACTACATATCAAGATATCTTAGGAGCTC 300
Db 300 CAGACGTAGACAAATCCCATTCACCCCTACTATACATTAAGGACATCTTAGGGGCC 359
QY 301 TACTATTAATTTAAACCTCATGCTTCTAGTCTTAATTTCTCAGCGAGCTGCTGGAGACC 360
Db 360 TCTTACTAATTTAGCTCTAATACTACTAGTACTAATTCGACCCGACCTCTCTGGAGACC 419
QY 361 CAGACACTATACACGAGAAACCACTTAATACACCCACATATCAAGCCGGAATGAT 420
Db 420 CAGATAACTACACCCGAGCAATCCATCAACACCCCTCATCAAAACCCGAGTAT 479
QY 421 ACTTCTTATTGGATAGCAATCTCCGATCAATTTCTTAACAACTAGGAGG 472
Db 480 ACTTCTTATTGGATAGCAATCTTAGATCAATCCCCACAACTAGGAGG 531

RESULT 8

CB439091 728 bp mRNA linear EST 25-MAR-2003
LOCUS 680000 MARC 6BOV Bos taurus cDNA 5', mRNA sequence.
DEFINITION CB439091
ACCESSION CB439091.1 GI:29223751
VERSION EST.
KEYWORDS Bos taurus (cow)
SOURCE Bos taurus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
1 (bases 1 to 728)
Smith,T.P.L., Roberts,A.J., Echternkamp,S.E., Chitko-McKown,C.G.,
Wray,J.E. and Keele,J.W.
A second set of bovine ESTs from pooled-tissue normalized libraries
Unpublished (2003)
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and trimmed with the aid of the trim_alt option. Vector identified with cross_match v0.990329.
Plate: FQY8044 row: L column: 23
Seq primer: GTAATACGACTCACTATAGG.
Location/Qualifiers

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/tissue_type="pooled"
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/clone_lib="MARC 6BOV"
/note="Vector: pcDNA3.1; Site 1: EcoRI; Site 2: NotI; Library made with RNA pooled from multiple tissues including liver, lung, hypothalamus, pituitary, and placenta/endometrium."

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Query Match 76.6%; Score 361.6; DB 6; Length 728;
Best Local Similarity 85.4%; Pred. No. 3e-95;
Matches 403; Conservative 0; Mismatches 69; Indels 0; Gaps 0;
QY 1 TACCATGAGGACAAATATCTTTTGGAGGACACAGTCATCACCAATCTCTTCAGCAA 60
Db 44 TACCATGAGGACAAATATCTTTTGGAGGACACAGTCATCACCAATCTTTATCAGCAA 103
QY 61 TCCCATACATCGGTACAAACCTAGTAGAATGAATCTGAGGAGGTTCTCAGTAGATAAAG 120
Db 104 TCCCATACATCGGCACAAATTTAGTCGAATGAATCTGAGGCGGATTCTCAGTAGACAAAG 163
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Db 164 CAACCTTACCCGATTTTCGCCTTCACATTTTATCTCCATTTATCATTCATGCAATG 223
QY 181 CCATAGTACACCTACTGTTTCTCCAGAAACAGGATCCAAACCCACACAGGAATCTCAT 240
Db 224 CCATAGTACACCTACTGTTTCTCCAGAAACAGGATCCAAACCCACACAGGAATTTCT 283
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QY 301 TACTATTAATTTAAACCTCATGCTTCTAGTCTTAATTTCTCAGCGAGCTGCTGGAGACC 360
Db 344 TCTTACTAATTTAGCTCTAATACTACTAGTACTAATTCGACCCGACCTCTCTGGAGACC 403
QY 361 CAGACACTATACACGAGAAACCCACTTAATACACCCACATATCAAGCCGGAATGAT 420
Db 404 CAGATAACTACACCCGAGCAATCCATCAACACCCCTCATCAAAACCCGAGTAT 463
QY 421 ACTTCTTATTGGATAGCAATCTCCGATCAATTTCTTAACAACTAGGAGG 472
Db 464 ACTTCTTATTGGATAGCAATCTTAGATCAATCCCCACAACTAGGAGG 515

RESULT 9

CN824188 863 bp mRNA linear EST 02-JUN-2004
LOCUS CN824188
DEFINITION Oa_splbn_07C24_M13reverse Sheep spleen\brain pSport1 library Ovis

aries cDNA clone Oa_sp1bn_07C24 5', mRNA sequence.
 ACCESSION CN824188
 VERSION CN824188.1 GI:47952257
 KEYWORDS EST.
 SOURCE Ovis aries (sheep)
 ORGANISM Ovis aries

REFERENCE 1 (bases 1 to 863)
 AUTHORS Gosner, A. and Hopkins, J.
 TITLE Ovine spleen/brain cDNA library
 JOURNAL Unpublished (2004)
 COMMENT Veterinary Biomedical Sciences
 University of Edinburgh
 Summerhall Square, Edinburgh, EH9 1QH.
 Email: j.hopkins@ed.ac.uk
 Plate: 07 row: C column: 24
 Seq primer: M13reverse
 High quality sequence start: 6
 High quality sequence stop: 550.

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 Best Local Similarity 86.0%; Pred. No. 1.8e-94;
 Matches 398; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

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 Db 461 TTCCATATTTGGACAAACCTAGTCGAATGAATCTGGGAGGATTCAGTAGACAAAG 520
 Oy 121 CAACCTTTACCGGATTTTTCGCTTCCACTTTATCTCCCTCCATTTATCATTCGAGCCCTTA 180
 Db 521 CTAGCCTCACCGGATTTTTCGCTTCCACTTTATTTTCCCATTCATCATCGAGCCCTCG 580
 Oy 181 CCATAGTACACTACTGTTTTCACGAAACAGGATCCAAACCCACAGGAATCTCAT 240
 Db 581 CCATAGTACACTACTGTTTTCACGAAACAGGATCCAAACCCACAGGAATCTCAT 640
 Oy 241 CAGACGACAGCAAAATTCATTTCCACCCCTACTACTATCAAGAGATATCTAGGAGTC 300
 Db 641 CGGACACAGATAAAATTCCTTCCACCTTATTAACCATTAAGACATCTAGTGCTA 700
 Oy 301 TACTATTAATTTAACTCATGTTCTAGTCTTCTTCTCAGGAGCTGTTTCGAGAGCC 360
 Db 701 TCTTACTAATCTCATCTCTATGCTACTAGTACTATTTCAGCCTGACTTACTCGAGACC 760
 Oy 361 CAGACACTATACACGAGCAACCCACTTAATACACCCCAATATCAAGCCCAATGAT 420
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 Oy 421 ACTTCTTATTTGCATAGGCAATCTCCGATCAATTCCTTAACAA 463
 Db 821 ACTTCTTATTTGCATAGGCAATCTTAGATCAATTCCTTAACAA 863

RESULT 10
 CB223436
 LOCUS 515 bp mRNA linear EST 10-FEB-2003
 DEFINITION l3EJ23E10 Bos taurus Jejunum #1 library Bos taurus cDNA, mRNA
 sequence.

ACCESSION CB223436
 VERSION CB223436.1 GI:28293950
 KEYWORDS EST.
 SOURCE Bos taurus (cow)
 ORGANISM Bos taurus

REFERENCE 1 (bases 1 to 515)
 AUTHORS Hansen, C., Fu, A., Meng, Y., Li, C., Okine, E., Sensen, C.W.,
 Gordon, P.M.K. and Moore, S.S.
 TITLE Gene Expression Profiling of the Bovine Gastrointestinal Tract
 JOURNAL Unpublished (2002)
 COMMENT Contact: Dr. Stephen Moore
 Beef Genomics Laboratory
 Dept of AFNS, University of Alberta
 410 Agri/For, Dept of AFNS, U of A, Edmonton, AB, T6G 2P5, Canada
 Tel: 780 492 0169
 Fax: 780 492 4265
 Email: stephen.moore@ualberta.ca
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FEATURES
 Location/Qualifiers
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 /cell_type="Simple columnar epithelial"
 /dev_stage="Young adult"
 /lab_host="XL1-BlueMRF'strain"
 /clone_lib="Bos taurus Jejunum #1 library"
 /note="Organ: Intestine/Jejunum; Vector: Uni-2ZAPXR;
 Site_1: EcoRI; Site_2: Xho I"

ORIGIN

Query Match 75.3%; Score 355.6; DB 6; Length 515;
 Best Local Similarity 85.2%; Pred. No. 1.6e-93;
 Matches 397; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

Oy 1 TACCATGAGGACAAATATCTTTTGGAGGACAAAGTCATCACCAATCTCTTTTCAGCAA 60
 Db 50 TACCATGAGGACAAATATCTTTGAGGAGCAACAGTCATCACCAATCTCTTTTCAGCAA 109
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 Db 110 TCCCATACATCGGCACAAATTTAGTGAATGAATCTGAGGAGGTTCTCAGTAGACAAAG 169
 Oy 121 CAACCTTTACCGGATTTTTCGCTTCCACTTTATCTCCCTCCATTTATCATTCGAGCCCTTA 180
 Db 170 CAACCTTTACCGGATTTTTCGCTTCCACTTTATCTCTTCCATTTATCATCATGCAATG 229
 Oy 181 CCATAGTACACTACTGTTTTCACGAAACAGGATCCAAACCCACAGGAATCTCAT 240
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 Oy 241 CAGACGACAGCAAAATTCATTTCCACCCCTACTACTATCAAGATATCTAGAGCTC 300
 Db 290 CAGACGTAGCAAAATTCCTTCCACCCCTACTACTATCAAGATATCTTAGGAGCTC 349
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 Db 350 TCTTACTAATTTAGCTCTAATCTACTAGTACTATTTCGACCCGAGCTCTCTCGAGACC 409
 Oy 361 CAGACAACTATACACGAGCAACCCACTTAATACACCCCAATATCAAGCCCAATGAT 420
 Db 410 CAGATAACTACACCCGAGCAATCCACTCAACACACCCCTCATCAACACCCGAGTAT 469
 Oy 421 ACTTCTTATTTGCATAGGCAATCTCCGATCAATTCCTTAACAACT 466
 Db 470 ACTTCTTATTTGCATAGGCAATCTTAGATCAATTCCTTAACAACT 515

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RESULT 11
CB220605
LOCUS      1Abo24C06 Bos taurus Abomasum #1 library Bos taurus cDNA, mRNA
DEFINITION
sequence.
ACCESSION  CB220605
VERSION     CB220605.1
KEYWORDS   EST.
SOURCE     Bos taurus (cow)
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
REFERENCE  1 (bases 1 to 552)
AUTHORS   Hansen, C., Fu, A., Meng, Y., Li, C., Okine, E., Senses, C.W.,
Gordon, P.M.K. and Moore, S.S.
TITLE     Gene Expression Profiling of the Bovine Gastrointestinal Tract
JOURNAL   Unpublished (2002)
COMMENT   Contact: Dr. Stephen Moore
Beef Genomics Laboratory
Dept of AFNS, University of Alberta
410 Agri/For, Dept of AFNS, U of A, Edmonton, AB, T6G 2P5, Canada
Tel: 780 492 0169
Fax: 780 492 4265
Email: stephen.moore@ualberta.ca
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FEATURES             Location/Qualifiers
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                     /lab_host="XLI-BlueMRP'-strain"
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                     I; Site_2: Xho I"

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Query Match      75.3%; Score 355.6; DB 6; Length 552;
Best Local Similarity 85.2%; Pred. No. 1.6e-93;
Matches 397; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

QY  1  TACCATGAGGACAAATATCTTTTGAGGAGCAACAGTCATCACAAATCTCTTCAGCAA 60
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QY  61  TCCCATACATCGGTACAACTAGTAGAATGATCTGAGGAGGTTCTCAGTAGATAAAG 120
DB  147  TCCCATACATCGGCACAAATTTAGTGAATGAATCTGAGGCGGATTCTCAGTAGACAAAG 206
QY  121  CAACCCCTTACCGATTTTTCGCCCTTCCACTTTATCTCTCCCATTTATCATTCGAGCCCTTA 180
DB  207  CAACCCCTTACCGATTTTTCGCCCTTCCACTTTATCTCTCCCATTTATCATTCAGCAATTG 266
QY  181  CCATAGTACACCTACTGTTTCTCCAGAAACAGGATCCAAACCCCAAGGAAATCTCAT 240
DB  267  CCATAGTCCACCTACTATTCTCCAGAAACAGGCTCCAAACCCCAAGGAAATTTCTCT 326
QY  241  CAGAGGAGACAAATTCATTCACCCCTACTACTACTATCAAGATATCTTAGAGCTC 300
DB  327  CAGAGGTAGACAAATCCATTCACCCCTACTACTACTATTAAGGACATCTTAGGGCCC 386
QY  301  TACTATTAAATTTAAACCTCATGCTTCTAGTCTTATCTACCGGAGCTGCTCGAGACC 360
DB  387  TCTTACTAAATCTAGTCTTAATACTACTAGTACTATTCGACCCGAGCTCTCTCGAGACC 446
QY  361  CAGACAACTATACACGCAACCCACTTATATACACCCCAATATCAAGCCCGAATGAT 420
DB  447  CAGATNACTACACCCGACCAATCCACTCAACACACACCCCTCACATCAAAACCCGAGTAT 506

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QY  421  ACTTCCTATTTCATACGCAATCTCCGATCAATTCCTTAACAACT 466
DB  507  ACTTCTATTTCATACGCAATCTTACGATCAATCCCAACAACT 552

RESULT 12
CR451416
LOCUS      735 bp mRNA linear EST 02-JUL-2004
DEFINITION  CR451416 Day 14 bovine embryos (bcail) Bos taurus cDNA clone
sequence.
ACCESSION  CR451416
VERSION     CR451416.1
KEYWORDS   EST.
SOURCE     Bos taurus (cow)
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
REFERENCE  1 (bases 1 to 735)
AUTHORS   Renard, J.P., Sreenan, J.P. and Hue, I.
TITLE     Embryonic ESTs (bcail)
JOURNAL   Unpublished (2004)
COMMENT   Contact: Renard JP
Biologie du Développement et Reproduction
INRA
Domaine de Vilvert 78350 Jouy en Josas, FRANCE
Email: renard@jouy.inra.fr
Funding for EST sequencing was provided by an INRA funding
(AIPPO0183). Funding for the cDNA library construction was provided
by an EEC contract (BO14-CT95-0190).
The library was constructed by I. Hue, BDR, INRA, 78350
JOUY-EN-JOSAS. The double stranded cDNA was un-directionally cloned
in a TA cloning vector. bcail is a SMART cDNA library. Insert size
was between 450 and 3500 bp. Sequencing was done from the 5' end of
the clone.
Sequence cleaned of vector, adaptor and repetitions. Contact us
at signenasupport@jouy.inra.fr to obtain the chromatogram of this
sequence.

FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
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                     /clone="bcail0012a.h.09"
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                     /notes="Vector: pCR2.1 (Invitrogen); Clone distribution :
                     AGENAE Resource centre. Francois PIUMI,
                     Francois.Piumi@jouy.inra.fr, INRA, CEA Radiobiologie et
                     Etude du genome (LREG), Domaine de Vilvert, 78352,
                     Jouy-en-Josas cedex, FRANCE, +33 (0) 1.34.65.28.02, +33
                     (0) 1.34.65.22.73"

ORIGIN
Query Match      75.3%; Score 355.6; DB 7; Length 735;
Best Local Similarity 85.3%; Pred. No. 1.7e-93;
Matches 397; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

QY  7  GAGACAAATATCTTTTGAGGAGCAACAGTCATCACCAATCTCTTCAGCAATCCCAT 66
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QY  67  ACATCGGTACAAACCTTAGTAGAATGAATCTGAGAGGGTTCTCAGTAGATAAGCAACCC 126
DB  61  ACATCGGCACAAATTTAGTCGAATGAATCTGAGGCGGATTCTCAGTAGACAAAGCAACCC 120
QY  127  TTACCCGATTTTCGCCCTTCCACTTTATCTCCCATTTATCATTCAGCCCTTACCATAG 186
DB  121  TTACCCGATTTTCGCCCTTCCACTTTATCTCCCATTTATCATTCAGCAATGCCCATAG 180
QY  187  TAGACCTACTGTTTCTCCACGAAACAGGATCCCAACACCCCAAGGAATCTCATCAGACG 246

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181 TCCACCTACTATTTCTCCAGGAAACAGGCTCCACAAACCAACAGGAATTTCTCAGAGC 240
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307 TAAATTTTAACTCCTAGTCTTAGTCTTCTCAGGACCTGCTTGGAGACCCAGACA 366
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361 ACTACACCCAGCAACCCCTTATACACACACCCCTTATACCAATCAAGGAGTCTTCT 420
427 TATTTGATACCAATCTCTCCGATCAATTCCTTAAACAACTAGGAGG 472
421 TATTTGATACCAATCTTACGATCAATTCCTTAAACAACTAGGAGG 466

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RESULT 13
CN789904
LOCUS 4124424 BARC 8BOV Bos taurus cDNA clone 8BOV_35C22 5', mRNA
DEFINITION CN789904 648 bp mRNA linear EST 26-MAY-2004
ACCESSION CN789904
VERSION CN789904.1 GI:47685884
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
1 (bases 1 to 648)
Baumann,R.G.; Baldwin,R.L.; Sonstegard,T.S.; Van Tassel,C.P. and
Matukumalli,L.K.
Construction and Analysis of a cDNA Library Generated From
Intestinal Muscle and Epithelial Tissues of Holstein Cattle
Unpublished (2004)
Contact: Richard G. Baumann
Bovine Functional Genomics Lab
ANRI
BLDG 162: BARC-EAST, Beltsville, MD 20705, USA
Tel: 3015048604
Fax: 3015048744
Email: rbaumann@anri.barc.usda.gov
Single pass sequencing. Bases called and trimmed with phred
0.000925 using options -trim_alt '' -trim fastaVector identified by
cross_match using options -minmatch 12 -minscore 12
Plate: 35 row: C column: 22
Seq primer: CCTATTAGTGACACTATAGAAC
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/lab_host="DH10B Tonk"
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/note="Organ: Intestine; Vector: pCMVSPORT6.1; Site 1:
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library in pCMVSPORT6.1, constructed from equimolar mRNA
pools derived from 5 sources, 4 lactating intestinal, 1
neonatal intestinal 4/5 lactating, Proximal Duodenum,
Jejunum, Distal Ileum, Colon, 1/5 Neonatal, Proximal
Duodenum, Jejunum, Distal Ileum"

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ORIGIN

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Query Match 75.2%; Score 355; DB 7; Length 648;
Best Local Similarity 85.0%; Pred. No. 2.5e-93;
Matches 397; Conservative 0; Mismatches 70; Indels 0; Gaps 0;
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QY 61 TCCCATATCATCGGTACAAACCTAGTAGAATGAATCTGAGGAGGGTTCTCAGTAGATAAAG 120
Db 242 TCCCATATCATCGGCAAAATTTAGTTCGAATGAATCTGAGGCGGAATCTCAGTAGACAAAG 301
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QY 181 CCATAGTACACCTACTGTTTCTCCAGGAAACAGGATCCAAACACCCCAACAGCAATTTCT 240
Db 362 CCATAGTCCACCTACTGTTTCTCCAGGAAACAGGATCCAAACACCCCAACAGCAATTTCT 421
QY 241 CAGCGGAGACAAATTCATTCACCCCTACTACACTATCAAGATATCTTAGAGGCTC 300
Db 422 CAGACATAGACAAATTCATTCACCCCTACTACACTATCAAGATATCTTAGAGGCTC 481
QY 301 TACTATTATTTTAAACCCCTCATGCTTCTAGTCTTATCTCCCGGACCTGCTTGGAGACC 360
Db 482 TCTTACTAATTTCTAGCTCTTAATCTACTAGTACTATTCGACCCGACCTCTCTCGGAGACC 541
QY 361 CAGCAACTATACACCCAGCAACCCCTTATATACACCCCCCAATATCAAGCCCGCAATGAT 420
Db 542 CAGATAACTACACCCAGCAACCCCTTATATACACCCCCCAATATCAAGCCCGCAATGAT 601
QY 421 ACTTCCTATTTCATACGCAATCTCTCCGATCAATTCCTTAAACAACTA 467
Db 602 ACTTCCTATTTCATACGCAATCTTACGATCAATTCCTTAAACAACTA 648

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VERSION BM435329.1 GI:18457051
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
1 (bases 1 to 560)
Hansen,C., Fu,A.; Meng,Y., Li,C., Okine,E., Senses,C.W.,
Gordon,P.M.K. and Moore,S.S.
Gene Expression Profiling of the Bovine Gastrointestinal Tract
Unpublished (2002)
Contact: Dr. Stephen Moore
Beef Genomics Laboratory
Dept of AFNS, University of Alberta
410 Agri/For, Dept of AFNS, U of A, Edmonton, AB, T6G 2P5, Canada
Tel: 780 492 0169
Fax: 780 492 4265
Email: stephen.moore@ualberta.ca
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